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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:52 ; Search time 1606 Seconds
(without alignments)
11302.170 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195
Sequence: 1 aatccgaaagttctgcac.....catttcaccagcaagttc 2195

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.Main:*
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2: /cgn2_6/prodata/1/pubpna/US08_PUBCONB.seq:*
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8: /cgn2_6/prodata/1/pubpna/US10D_PUBCONB.seq:*
9: /cgn2_6/prodata/1/pubpna/US10E_PUBCONB.seq:*
10: /cgn2_6/prodata/1/pubpna/US11_PUBCONB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867.2	39.5	898	5	US-10-011-672-35
2	867.2	39.5	898	5	US-10-012-070A-50
3	862.6	31.1	762	7	US-10-437-963-33718
4	136.8	6.12	3221	7	US-10-437-963-7912
5	126.8	5.8	719	9	US-10-487-901-2760
6	126.8	5.8	725	9	US-10-487-901-6610
7	126.8	5.8	808	7	US-10-260-238-51
8	120.2	5.5	781	7	US-10-437-963-7907
9	84.2	3.8	195	7	US-10-437-963-79997
10	77.4	3.5	294	7	US-10-437-963-49995
11	64.4	2.9	165	7	US-10-437-963-10222
12	59.6	2.7	213	7	US-10-437-963-54806
13	55.6	2.5	101954	7	US-10-322-281-782
14	55.4	2.5	8056	8	US-10-473-126-386
15	55.4	2.5	3673778	6	US-10-312-841-1
16	55.2	2.5	5379	6	US-10-311-455-1649
17	55.2	2.5	5379	6	US-10-240-485-129
18	55	2.5	69081	5	US-10-087-192-1132
19	54.4	2.5	16766	6	US-10-311-455-2129
20	53.8	2.5	9760	7	US-10-221-613-113
21	53	2.4	1243	8	US-10-425-115-172717
22	52.6	2.4	8076	7	US-10-257-166-36
23	52.6	2.4	8136	6	US-10-311-455-528

C	24	52.6	2.4	8136	7	US-10-257-166-38	Sequence 38, Appl
C	25	52.6	2.4	158001	7	US-10-211-179-11	GENERAL INFORMATION
C	26	52.4	2.4	3673778	6	US-10-312-841-1	Sequence 1, Appl
C	27	51.6	2.4	8056	8	US-10-473-126-240	Sequence 240, Appl
C	28	51.6	2.4	147300	9	US-10-723-681-3	Sequence 3, Appl
C	29	51.4	2.3	5979	5	US-10-239-676-18	Sequence 18, Appl
C	30	51.4	2.3	5979	5	US-10-240-453-26	Sequence 26, Appl
C	31	51.4	2.3	7941	7	US-10-433-793-139	Sequence 139, Appl
C	32	51.2	2.3	998	3	US-09-816-894-5	Sequence 5, Appl
C	33	51.2	2.3	7374	7	US-10-257-166-117	Sequence 117, Appl
C	34	51	2.3	14095	6	US-10-311-455-450	Sequence 450, Appl
C	35	50.8	2.3	15732	5	US-10-239-676-95	Sequence 95, Appl
C	36	50.8	2.3	15732	6	US-10-240-453-107	Sequence 107, Appl
C	37	50.6	2.3	6131	6	US-10-311-455-863	Sequence 863, Appl
C	38	50.2	2.3	16766	6	US-10-311-455-2130	Sequence 2130, Appl
C	39	50.2	2.3	50000	8	US-10-706-635-24	Sequence 24, Appl
C	40	50	2.3	7001	5	US-10-172-086-60	Sequence 60, Appl
C	41	50	2.3	7001	7	US-10-311-507-2	Sequence 2, Appl
C	42	50	2.3	7001	6	US-10-480-846-60	Sequence 60, Appl
C	43	50	2.3	7276	6	US-10-311-455-875	Sequence 875, Appl
C	44	50	2.3	14006	6	US-10-311-455-1931	Sequence 1931, Appl
C	45	50	2.3	18683	6	US-10-311-455-285	Sequence 285, Appl

ALIGNMENTS

RESULT 1
US-10-011-672-35
US-10-011-672-35
Sequence 35, Application US/10011672
Publication No. US20030049814A1
GENERAL INFORMATION:
APPLICANT: Hawker, Timothy
APPLICANT: Warner, Simon
APPLICANT: Andrews, Christopher
APPLICANT: Bachoo, Savinder
APPLICANT: Pickett, Andrew
TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
FILE REFERENCE: 50489/UST
CURRENT APPLICATION NUMBER: US/10/011,672
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/GB00/01559
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 35
LENGTH: 898
TYPE: DNA
ORGANISM: Oryza sp.
US-10-011-672-35

Query Match 39.5%; Score 867.2; DB 5; Length 898;
Best Local Similarity 99.2%; Pred. No. 8.6e-186;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

1 AATCGGAAAGTTTGCACCGTTTCAAGTCTAATCAATATAGGAAAGTGTCT 60
2 AATCGGAAAGTTTGCACCGTTTCAAGTCTAATCAATATAGGAAAGTGTCT 61
61 AATATTAATTAAGACCTTATATATATGACGCTGATTAAGAACTATATGA 120
62 AATATTAATTAAGACCTTATATATATGACGCTGATTAAGAACTATATGA 121
121 CATTCAACCTTATGTTGCGCATCGGGCTAATTAATTAAGAACTGCTAGTT 180
122 CATTCAACCTTATGTTGCGCATCGGGCTAATTAATTAAGAACTGCTAGTT 181
181 TTTCCTTAGTATTAAGTGGGAAATGAATCAATATTGCTTAGAATATACCT 240
182 TTTCCTTAGTATTAAGTGGGAAATGAATCAATATTGCTTAGAATATACCT 241
241 TTTCCTTAGTATTAAGTGGGAAATGAATCAATATTGCTTAGAATATACCT 300

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Db      242 TCTGTCATGAAGTTAAATTAATTCGAGGTAGCCATAATGTGCATCAAACTCTCTTGAAATA 301
Qy      301 AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTAAAAAATAAAT 360
Db      302 AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTT---AAAAAAT 358
Qy      361 AGAATGAAGATATTTCTGAACGTATCGGCAAAAGTTTAAACATATTAATTAATTTAT 420
Db      359 AGAATGAAGATATTTCTGAACGTATCGGCAAAAGTTTAAACATATTAATTAATTTAT 418
Qy      421 AGTTGTGATTCGTATATTCGACGTCAATTAGGACATGCTTACTCATCTCAATTTT 480
Db      419 AGTTGTGATTCGTATATTCGACGTCAATTAGGACATGCTTACTCATCTCAATTTT 478
Qy      481 TATTTAGTAAATTAAGACATTAATTTATTTTATTTATTTTTCGATTAGATGC 540
Db      479 TATTTAGTAAATTAAGACATTAATTTATTTTATTTATTTTTCGATTAGATGC 538
Qy      541 AAGGTACTTACGACACACTTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 599
Db      539 AAGGTACTTACGACACACTTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 598
Qy      600 CGTTCAACTAGGACACATCTCCAAATATGCACTCGCTATTTAATAATTAGTAGCAAT 659
Db      599 CGTTCAACTAGGACACATCTCCAAATATGCACTCGCTATTTAATAATTAGTAGCAAT 658
Qy      660 ATCTGAATTAAGACACTTCAACATCAGACACCACTTTTAATTAATCTAAATACAAA 719
Db      659 ATCTGAATTAAGACACTTCAACATCAGACACCACTTTTAATTAATCTAAATACAAA 718
Qy      720 AATTAATTTTACAGATAGCATGAAAAGTATGAAAAGCACTATTAGGTTTTCACATACA 779
Db      719 AATTAATTTTACAGATAGCATGAAAAGTATGAAAAGCACTATTAGGTTTTCACATACA 778
Qy      780 AAAAAAATTAAGATTTTGTCTCGCGCGGAGCGCCATCTCCCATTTTGGGACACAGGCA 839
Db      779 AAAAAAATTAAGATTTTGTCTCGCGCGGAGCGCCATCTCCCATTTTGGGACACAGGCA 838
Qy      840 ACAACAGAGTGCGTGGCCCAAGAACCAACCAAAAAAGATGATTTAAGGAGAGCAGC 899
Db      839 ACAACAGAGTGCGTGGCCCAAGAACCAACCAAAAAAGATGATTTAAGGAGAGCAGC 898

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RESULT 2
US-10-012-070A-50
; Sequence 50, Application US/10012070A
; Publication No. US20030077801A1
; GENERAL INFORMATION:
; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Andrews, Christopher
; APPLICANT: Bachoo, Savinder
; APPLICANT: Pickerill, Andrew
; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/GB00/01573
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Oryza sp.
US-10-012-070A-50

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Query Match      39.5%; Score 867.2; DB 5; Length 898;
Best Local Similarity 99.2%; Pred. No. 8.6e-186;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;
Qy      1 AATCGAAAAGTTTTCGACCGTTTACGTCCTTAACATATATAGGAAAGTGTGCT 60

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Db      2 AATCGAAAAGTTTTCGACCGTTTTCAGTTCTTAACATATATAGGAAAGTGTGCT 61
Qy      61 AATATATAATAGACCTTATATATATAGCGGTGATTAACATATATAGGAAAGT 120
Db      62 AATATATAATAGACCTTATATATATAGCGGTGATTAACATATATAGGAAAGT 121
Qy      121 CATTCACCTTACTTTTGTGGCAATCGGGCTAAATATAAAGAGTCCGTACACTAGTTTGT 180
Db      122 CATTCACCTTACTTTTGTGGCAATCGGGCTAAATATAAAGAGTCCGTACACTAGTTTGT 181
Qy      181 TTTCCTTATTAATTAAGTGGGAAATGAATCATTAATGCTTAAATATATAGTACATC 240
Db      182 TTTCCTTATTAATTAAGTGGGAAATGAATCATTAATGCTTAAATATATAGTACATC 241
Qy      241 TCTGTCATGAAGTTAAATTAATTCGAGTAGCCATTAATGTCAATCAACTCTTGAATA 300
Db      242 TCTGTCATGAAGTTAAATTAATTCGAGTAGCCATTAATGTCAATCAACTCTTGAATA 301
Qy      301 AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTAAAAAATAAAT 360
Db      302 AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTT---AAAAAAT 358
Qy      361 AGAATGAAGATATTTCTGAACGTATCGGCAAAAGTTTAAACATATTAATTAATTTAT 420
Db      359 AGAATGAAGATATTTCTGAACGTATCGGCAAAAGTTTAAACATATTAATTAATTTAT 418
Qy      421 AGTTGTGATTCGTATATTCGACGTCAATTAAGGACATGCTTACTCATCTCAATTTT 480
Db      419 AGTTGTGATTCGTATATTCGACGTCAATTAAGGACATGCTTACTCATCTCAATTTT 478
Qy      481 TATTTAGTAAATTAAGACATTAATTTTATTTTATTTATCTTTTTCGATTAGATGC 540
Db      479 TATTTAGTAAATTAAGACATTAATTTTATTTTATTTATCTTTTTCGATTAGATGC 538
Qy      541 AAGGTACTTACGACACACTTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 599
Db      539 AAGGTACTTACGACACACTTTGTGCTCATGTGCAATGTGAGTGCACCTCTC-ATACA 598
Qy      600 CGTTCAACTAGGACACATCTCCAAATATGCACTCGCTATTTAATAATTAGTAGCAAT 659
Db      599 CGTTCAACTAGGACACATCTCCAAATATGCACTCGCTATTTAATAATTAGTAGCAAT 658
Qy      660 ATCTGAATTAAGACCTTCAACATCAGACACCACTTTTAATTAATCTAAATACAAA 719
Db      659 ATCTGAATTAAGACCTTCAACATCAGACACCACTTTTAATTAATCTAAATACAAA 718
Qy      720 AATTAATTTTACAGATAGCATGAAAAGTATGAAAAGCACTATTAGGTTTTCACATACA 779
Db      719 AATTAATTTTACAGATAGCATGAAAAGTATGAAAAGCACTATTAGGTTTTCACATACA 778
Qy      780 AAAAAAATTAAGATTTTGTCTCGCGCGGAGCGCCATCTCCCATTTTGGGACACAGGCA 839
Db      779 AAAAAAATTAAGATTTTGTCTCGCGCGGAGCGCCATCTCCCATTTTGGGACACAGGCA 838
Qy      840 ACAACAGAGTGCGTGGCCCAAGAACCAACCAAAAAAGATGATTTAAGGAGAGCAGC 899
Db      839 ACAACAGAGTGCGTGGCCCAAGAACCAACCAAAAAAGATGATTTAAGGAGAGCAGC 898

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RESULT 3
US-10-437-963-33718
; Sequence 33718, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbausk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33718
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(762)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37802C.1
US-10-437-963-33718

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Query Match      31.1%; Score 682.6; DB 7; Length 762;
Best Local Similarity 97.6%; Pred. No. 5.2e-144;
Matches 745; Conservative 0; Mismatches 11; Indels 7; Gaps 5;

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QY 1036 CCAAGAGAGGAGGAGACCAAGAGACGAGCTAGAGAGCGGAGCGGCTCTT 1095
DB 4 CGAGGAGAGGAGGAGACCAAGAGACGAGCTAGAGAGCGGAGCGGAGCGGCTCTT 62
QY 1096 CGATCCATATCTTCCGCGTGAAGTCTTGATGATCTTCCCTCTCACTCTCTCA 1155
DB 63 CGATCCATATCTTCCGCGTGAAGTCTTGATGATCTTCCCTCTCACTCTCTCA 122
QY 1156 CAGGGATATG---CCCTCGGTTGTTCTTGAGTTATGTTCTAGGTTGTGATGAG 1212
DB 123 CAGGGATATGCTCTCCCTCGGTTGTTCTTGAGTTATGTTCTAGGTTGTGATGAG 182
QY 1213 GGGTGAATGTTAGGAGAGGAGATCTGATCTGATGATCTCCGTTCTTGATGAGGAT 1272
DB 183 GCGTGAATGTTAGGAGAGGAGATCTGATCTGATGATCTCCGTTCTTGATGAGGAT 242
QY 1273 AGAGGGGTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1332
DB 243 AGAGGGGTTCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 302
QY 1333 CGTCTGAGAGCTCTATGAGAAATGATGATGATGATGATGATGATGATGATGATGAT 1392
DB 303 CGTCTGAGAGCTCTATGAGAAATGATGATGATGATGATGATGATGATGATGATGAT 362
QY 1393 GTRACCTTTGTTGAGGTAATAATCAGAGCACCGGTATTTGTTGTTGTTGTTGTTGTT 1452
DB 363 GTRACCTTTGTTGAGGTAATAATCAGAGCACCGGTATTTGTTGTTGTTGTTGTTGTT 421
QY 1453 CATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1512
DB 422 CATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 481
QY 1513 TTTATTCCTATTTGAACAAAATATCAACTTTGAAAGCGGTCCGTTGATGAGATGA 1572
DB 482 TTTATTCCTATTTGAACAAAATATCAACTTTGAAAGCGGTCCGTTGATGAGATGA 541
QY 1573 ATGATGATTTCTTAAGCTCTGCAAAATTTGCAAGTGGCTGTTTGAATACATGATGTC 1632
DB 542 ATGATGATTTCTTAAGCTCTGCAAAATTTGCAAGTGGCTGTTTGAATACATGATGTC 601
QY 1633 CCATCCAGAAATTCATGAAATAGTATATCTCTGAGAAACAGGGGATCCCGTTCTTC 1692
DB 602 CCATCCAGAAATTCATGAAATAGTATATCTCTGAGAAACAGGGGATCCCGTTCTTC 661
QY 1693 CGATTTGCTTTAGTCCAGAAATTTTTCCTCAATATCTTTAAAGATCACTTCTGAT 1752
DB 662 CGATTTGCTTTAGTCCAGAAATTTTTCCTCAATATCTTTAAAGATCACTTCTGAT 720
QY 1753 CAGTTCAATGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1795
DB 721 CAGTTCAATGATGATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 762

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RESULT 4
US-10-437-963-7912
; Sequence 7912, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 7912
; LENGTH: 3221
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14463C.1
US-10-437-963-7912

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Query Match      6.2%; Score 136.8; DB 7; Length 3221;
Best Local Similarity 89.8%; Pred. No. 4.7e-20;
Matches 158; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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QY 988 TAAATATCTCTCCCTCTTCTCTCTATATGAGAGCATTCAGGCAAGAGAGG 1047
DB 221 TAAATATCTCTGGTCTCACTCTCCCTCGATATGAGAGCATTCAGGCAAGAGAGG 280
QY 1048 AGAGCACCAAGAGACGCGACTAGAGAGAGCGGAGCGGCTTCTTGATCATATCT 1107
DB 281 AGAGCACCAAGAGACGCGACTAGAGAGAGCGGAGCGGCTTCTTGATCATATCT 339
QY 1108 TCCGGTCCAGTTCTTGTGATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1163
DB 340 TCCGGTCCAGTTCTTGTGATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 395

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RESULT 5
US-10-487-901-2760
; Sequence 2760, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreary, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Meglarz, Thadeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrimus, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crooley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteri
; FILE REFERENCE: DOW-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2760
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic

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Query Match      5.5%; Score 120.2; DB 7; Length 781;
Best Local Similarity 90.3%; Pred. No. 1.3e-16;
Matches 139; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 1010 CCTCTCTATATGAGGACATCCAGCCAGAAAGAGGAGAGACCAAGACGCGACT 1069
    |||||
DB 243 CCGGCCGATATACGAGGATCCAGGCCAGAAAGAGGAGAGACCAAGACGCGACT 302
    |||||

QY 1070 AGCAGAACCGAGACGCGCCTTCTTCATCATATCTTCGGTTCGATCTTGTCAT 1129
    |||||
DB 303 AGCAGAACCGAGACGCGC-NTTCTCTGTTTCATATCTTCGGTTCGATCTTGTCAT 361
    |||||

QY 1130 CTCTTCCTCTCTCCACTCTCTCTCTCAAGGGTAT 1163
    |||||
DB 362 CTCTTCCTCTCTCACTCTCTCTCTCAAGGGTCT 395
    |||||

RESULT 9
US-10-437-963-79997
; Sequence 79997, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 79997
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79665C.1
US-10-437-963-79997

Query Match      3.8%; Score 84.2; DB 7; Length 195;
Best Local Similarity 82.0%; Pred. No. 9.2e-09;
Matches 109; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 1031 CCAAGCCAGAAAGAGGAGAGACCAAGACGCGACTAGCAGAGCCGAGCGGC 1090
    |||||
DB 28 CCAATGAAAGAAAGAGGAGAGACGAGCATGACACTCCATGATGAAAGCCGAGCGGC 87
    |||||

QY 1091 TTCTTCGATCATATATCTTCGGTTCGATCTTGTCATCTTCCCTCCACTCTCT 1150
    |||||
DB 88 TT-ATCTATCCATATATCTTCGGTTCGATCTTGTCATCTTGTCATCTCTCTCT 146
    |||||

QY 1151 CCTCAGAGGTAT 1163
    |||||
DB 147 CCTGACAGGTCT 159
    |||||

RESULT 10
US-10-437-963-49995
; Sequence 49995, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
```

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; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49995
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(294)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52525C.1
US-10-437-963-49995

Query Match      3.5%; Score 77.4; DB 7; Length 294;
Best Local Similarity 87.6%; Pred. No. 3.9e-07;
Matches 92; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1059 GACAGCGACTAGCAGAAAGCCGAGCGCCTTCTTCATCATATCTTCGTCGAGT 1118
    |||||
DB 7 GCCAGACGACTAGCAGAAAGCCGAGCGACCCNNC-TCCTGATCATATCTTCGTCGAGT 65
    |||||

QY 1119 TCTTGTCATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1163
    |||||
DB 66 TCTTGTCATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 110
    |||||

RESULT 11
US-10-437-963-10222
; Sequence 10222, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 10222
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16565C.1
US-10-437-963-10222

Query Match      2.9%; Score 64.4; DB 7; Length 165;
Best Local Similarity 80.0%; Pred. No. 0.00026;
Matches 88; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

QY 1054 CCAAGACACGCGACTAGCAGAAAGCCGAGCGCCTTCTTCATCATATCTTCGGT 1113
    |||||
DB 5 CAAAGTACACTCTACTAGCATTAAGCCGATCGACCGCTTTC-TCGATCATATCTTCGGT 63
    |||||

QY 1114 CGAGTTCTTGTCATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1163
    |||||
DB 64 GGAGTTCTTGTCATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 113
    |||||
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Db      6717 TAAATCAACATTATAAACATAAAAAATTTATTTTAAATTAATTAATAAAATT 6658
Qy      690 ACCACTTTTAAATATATCTAAAAATACAAAAATATAATTTTACAGATAGCATGAAGTAT 749
        |||||
Db      6657 AAAAATTTCAATATAAAAAATATAAAAAATATAAACATATAATTAATTAATAAAATA 6598
Qy      750 GAAACGAACTATTAGCTTTTTCACATACAAAAAAAAGAAATTT 796
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Db      6597 ATAAATTTTTCATTTTAATTTAAATTTAAATTAATAATATATAT 6551
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RESULT 15

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US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: EpiGenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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Query Match      2.5%; Score 55.4; DB 6; Length 3673778;
Best Local Similarity 53.7%; Pred. No. 4.8; Indels 2; Gaps 1;
Matches 137; Conservative 0; Mismatches 116;
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Qy      327 GGGTAAAGAGATATTTTAAAAAATAGATGAGATATCTGAACGTATCG 386
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Db      2720210 GGTAAATAGAGCGAGATTTATTTAAAAAAGAAATATTTGTTTTTT 2720269
Qy      387 GCAAAGATTAAACATATATATATATATTTATAGTTGGCATTCGTTATTCGCACG 446
        |||||
Db      2720270 TTAATAGTTTAA--GTTTACGGTATATGTATACGTAGCTTGTATATATATAT 2720327
Qy      447 TCATTAAGSACATGCTTCTCATCTCAATTTTATTTAGTAATTAAGACATTTGACT 506
        |||||
Db      2720328 AATATGTTACGTGTGTGTGATTTATTTTATTAATTAATTAAGTATATTTT 2720387
Qy      507 TATTTTATTTATTTATCTTTTTCGATTAAGATGACAGTACTTACGCACACTTTGTGC 566
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Db      2720388 AATGTTATTTTATTTTATTTTATTTTATTAATTAATGTTTATAGTGTAAAGTTT 2720447
Qy      567 TCATGTGATGTGTG 581
        |||||
Db      2720448 TTTTGTGTTATGTG 2720462
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Search completed: April 21, 2006, 09:26:22
Job time : 1614 secs
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Db 893 AAAATCAGACCGCGGATTTTGGCTGTATAAAGTACCGGCTTGCCCTCGA 835

1471 TTCTGGTAGTATGCTTCCTGATTTGACAGAGCTATCTTTGTTATTCCTATTGACA 1530
|
|
|
834 TTCTGGTAGTATGCTTCCTGATTTGACAGAGCTATCTTTGTTATTCCTATTGACA 775
|
|
|
1531 AAAATTAATCACTTTGAAGACGGTCCCGTGAATGATTTGAATGATTTCTTAAG-C 1589
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|
|
774 AAAATTAATCACTTTGAAGACGGTCCCGTGAATGATTTGAATGATTTCTTAAGC 715
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1590 CTGTCCAAATTTGCGAGCTGCTGTTTATGATACAGTATGCCCATCAGAAATTCAG 1649
|
|
|
714 CTGTCCAAATTTGCGAGCTGCTGTTTATGATACAGTATGCCCATCAGAAATTCAG 655
|
|
|
1650 AAAACGTTATTAATCTCTCAGAAACAGGGATTCCTGTTCTTCGATTTGCTTAAGTCCC 1709
654 GAAACGTTATTAATCTCTCAGAA-----AATTCCTGTTCTTCGATTTGCTTAAGTCCC 600
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|
1710 AGAATTTTTCCTCCCAATTTCTTAATAAGTCACTTTGCTGCTCACTTCAATGAATGAT 1769
|
|
|
599 AGAATTTTTCCTCCCAATTTCTTAATAAGTCACTTTGCTGCTCACTTCAATGAATGAT 540
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1770 TGTCAAAATTAATGCTTTTATAGCGTTATCTTACGTATGCTGATTTAGGTAATACC 1829
539 TGTCAAAATTAATGCTTTTATAGCGTTATCTTACGTATGCTGATTTAGGTAATACC 480
|
|
|
1830 CCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCATTATTAATATG 1889
479 CCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCATTATTAATATG 420
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|
|
1890 AAATGAACGTGACATTAAGCATTAATCATTTGATTAATTTTATTTTATTTGCTTCACTCC 1949
419 AAATGAACGTGACATTAAGCATTAATCATTTGATTAATTTTATTTTATTTGCTTCACTCC 360
|
|
|
1950 TTCAATTTCTGAGCTGAAAGTCTGACATGAATCTGCTCAATTTGTTTCAATTTCAAC 2009
359 TTCAATTTCTGAGCTGAAAGTCTGACATGAATCTGCTCAATTTGTTTCAATTTCAAC 300
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2010 ATCGATTAATCTATGATTAATCTCTTGTATCTAATCTGTAAGATTTCTTTGTTATTC 2069
299 ATCGATTAATCTATGATTAATCTCTTGTATCTAATCTGTAAGATTTCTTTGTTATTC 240
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2070 CTGATCTGCTGATTAATCAAGAAATTTATGAAAGTGAATGCGGATGTTATTAATGCT 2129
239 CTGATCTGCTGATTAATCAAGAAATTTATGAAAGTGAATGCGGATGTTATTAATGCT 180
|
|
|
2130 TGTCTTAATGATTAATCTCTTGTGTCAGATTTCTGTTAGTATGCTCACTTCAACGACA 2189
179 TGTCTTAATGATTAATCTCTTGTGTCAGATTTCTGTTAGTATGCTTGCATCTTCAACGACA 120
|
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|
2190 AAGTT 2194
119 AAGTT 115
|
|
|
RESULT 2
LOCUS AU075848 716 bp mRNA linear EST 03-APR-2002
DEFINITION AU075848 Rice mature leaf *Oryza sativa* (japonica cultivar-group)
CDNA clone S20385_1A, mRNA sequence.
AU075848
ACCESSION AU075848.1 GI:5455455
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatroidae; Oryzaceae; *Oryza*.
1 (bases 1 to 716)
Yamamoto, K. and Sasaki, T.
Rice cDNA from mature leaf
Unpublished (1999)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tcsasaki@abr.affrc.go.jp, URL: http://rpg.dna.affrc.go.jp/
PROJECT = "RGP".
Location/Qualifiers
1. 716
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nippondare"
/db_xref="taxon:39947"
/clone="S20385_1A"
/issue_type="mature leaf"
/clone_1ib="Rice mature leaf"
ORIGIN
Query Match 29.3%; Score 642.8; DB 1; Length 716;
Best Local Similarity 97.8%; Pred No. 7.2e-133;
Matches 704; Conservative 0; Mismatches 9; Indels 7; Gaps 5;
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1079 CGAGGACCGCCCTTCCTGATCATATCTTCGGTCAAGTCTTGATCTCTCCCT 1138
1 CGAGGACCGCC-TCCTGATCATATCTTCGGTCAAGTCTTGATCTCTCCCT 59
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|
|
1139 CCTCACTCTCTCTCAAGGGTATG---CCCTTCGGTGTCTTGATTTATTTTC 1195
60 CCTCACTCTCTCTCAAGGGTATGCTCCCTTCGGTGTCTTGATTTATTTTC 119
|
|
|
1196 TAGGTGATGATACGGCGTTGATGTAAGAAAGGGATCTGATCTGATGATTCCT 1255
120 TAGGTGATGATACGGCGTTGATGTAAGAAAGGGATCTGATCTGATGATTCCT 179
|
|
|
1256 GTTCTTGATTTGGATTAAGAGGGGTTCTGATGTTGATGATTTGCTGTTGATTA 1315
180 GTTCTTGATTTGGATTAAGAGGGGTTCTGATGTTGATGATTTGCTGTTGATTA 239
|
|
|
1316 GATGATGATTTTCAATGCTCTGAGACTCTATAGGAATGAATNGTTTAGGGATCGGA 1375
240 GATGATGATTTTCAATGCTCTGAGACTCTATAGGAATGAATNGTTTAGGGATCGGA 299
|
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|
1376 ATCTGCGATTTTGGAGTACCTTTGTTAGGTAATGATGATGATGATTTGCTGATTT 1435
300 ATCTGCGATTTTGGAGTACCTTTGTTAGGTAATGATGATGATGATTTGCTGATTT 359
|
|
|
1436 TTGATGATTAATAAGTACATTTGTTGCTCTGATTTCTGATGATGATTTGCTGATTT 1495
360 TTGATGATTAATAAGTACATTTGTTGCTCTGATTTCTGATGATGATTTGCTGATTT 418
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|
1496 GACGAAGCTATCTTGTGTTATTCCTTAATGAAACAAATATCAACTTTGAAGACGT 1555
419 GACGAAGCTATCTTGTGTTATTCCTTAATGAAACAAATATCAACTTTGAAGACGT 478
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1556 CCCGTTGATGATTAAGTATGATTTCTTAAGCTGCTCAAAATTTTGCAGCTGGCTTG 1615
479 CCCGTTGATGATTAAGTATGATTTCTTAAGCTGCTCAAAATTTTGCAGCTGGCTTG 538
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1616 TTTAGATACAGTATGCTCCCATCAAGAAATTCATGAAACAGTTATTAATCTTCAAGACAG 1675
539 TTTAGATACAGTATGCTCCCATCAAGAAATTCATGAAACAGTTATTAATCTTCAAGACAG 598
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1676 GGGATTTCCCTGTTCTTCGATTTGCTTAATGCTCCCAATTTTCCCAATATCTTA 1735
599 GGGATTTCCCTGTTCTTCGATTTGCTTAATGCTCCCAATTTTCCCAATATCTTA 657
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1736 AAAGTCACTTCTGTTGATGATTAAGTATGATTTGCTTACAAATATCTTTATAGCGT 1795
658 AAAGTCACTTCTGTTGATGATTAAGTATGATTTGCTTACAAATATCTTTATAGCGT 716
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|
|
RESULT 3
LOCUS CF304397 627 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF1--04-N21.g1 ABF3-overexpressing transgenic rice lambda phage

cdna library (ABF1) *Oryza sativa* (japonica cultivar-group) cDNA
clone ABF1--04-N21, mRNA sequence.
CF304397
VERSION
CF304397.1 GI:33676158
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristidae; Oryzaceae; *Oryza*.
1 (bases 1 to 627)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 627
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--04-N21"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF1-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 26.2%; Score 575; DB 6; Length 627;
Best Local Similarity 98.4%; Pred. No. 1.1e-117;
Matches 613; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

1046 GGAAGACACCAAGACACCGGATGACGAAAGCCGACCGCTTCTGATCCATAT 1105
DB 7 GGAAGACACCAAGACACCGGATGACGAAAGCCGACCGCTTCTGATCCATAT 65
1106 CTTCCGGTGGAGTCTTGGTGCATCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 1165
DB 66 CTTCCGGTGGAGTCTTGGTGCATCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 125
1166 G--CCCTTGGTGGTCTTGGATTTATTTAGTTGATGATGATGATGATGATGAT 1222
DB 126 GCTCCCTTGGTGGTCTTGGATTTATTTAGTTGATGATGATGATGATGATGAT 185
1223 TAGAAAAGGGATCTGATCTGATGATGATCTGTTCTGGATTTGGATGATGAGGGGTTTC 1282
DB 186 TAGAAAAGGGATCTGATCTGATGATGATCTGTTCTGGATTTGGATGATGAGGGGTTTC 245
1283 TTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342
DB 246 TTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
1343 GCTCTATGGAATGAATGATTTAGGTAAGGATCTTGCGATTTTGTAGTACTTTTG 1402
DB 306 GCTCTATGGAATGAATGATTTAGGTAAGGATCTTGCGATTTTGTAGTACTTTTG 365
1403 TTTAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1462
DB 366 TTTAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 424

1463 GTCCTGATTTCTGGTAGTATGATCTTCTGATTTGACGAAGCTATCTTTGTTATTCCT 1522
DB 425 GTCCTGATTTCTGGTAGTATGATCTTCTGATTTGACGAAGCTATCTTTGTTATTCCT 484
1523 ATTGAACAAAATTAATCAACTTTGAAGACGGCCGCTTGATGATGATTAATGATGAT 1582
DB 485 ATTGAACAAAATTAATCAACTTTGAAGACGGCCGCTTGATGATGATTAATGATGAT 544
1583 CTTAAGCTGTCCAAATTTGCGAGCTGCTTTGATGATGATGATGATGATGATGATGAT 1642
DB 545 CTTAAGCTGTCCAAATTTGCGAGCTGCTTTGATGATGATGATGATGATGATGATGAT 604
1643 ATTCAATGAATCAATTAATATCC 1665
DB 605 ATTCAATGAATCAATTAATATCC 627

RESULT 4
CF306344 619 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HDAL--03-109.g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) *Oryza sativa* (japonica cultivar-group) cDNA
clone HDAL--03-109, mRNA sequence.
CF306344.1 GI:33678105
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriaristidae; Oryzaceae; *Oryza*.
1 (bases 1 to 619)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 619
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAL--03-109"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 25.8%; Score 566.8; DB 6; Length 619;
Best Local Similarity 98.1%; Pred. No. 7.2e-116;
Matches 606; Conservative 0; Mismatches 7; Indels 5; Gaps 3;

1036 CCAAGAAAGGAGAGACCAAGACACGACCTAGCAGAAAGCCGACCGCTTCTT 1095
DB 4 CCAAGAAAGGAGAGACCAAGACACGACCTAGCAGAAAGCCGACCGCTTCTT 62
1096 CGATTCATATCTTCCGGTGGAGTCTTGGTGCATCTTCCCTCCCTCCCTCTCTCA 1155

Db 63 CGATCCATATCTTCGGGTGAGTTCCTTGTCATCTCTCCCTCCACCTCTCTCA 122

Qy 1156 CAGGGATATG--CCCTTCGGTGTCTTGAATTTATGTTAGTGTGTAGTACGG 1212

Db 123 CAGGGATATGCTCCCTTCGGTGTCTTGAATTTATGTTAGTGTGTAGTACGG 182

Qy 1213 GCGTTGATGTAGAAAAGGAGATCTGTATCTGTAGATGATTCCTGTTCTTGATTTGGAT 1272

Db 183 GCGTTGATGTAGAAAAGGAGATCTGTATCTGTAGATGATTCCTGTTCTTGATTTGGAT 242

Qy 1273 AGAGGGGTTCTTGATGTAGATGATTCGGTTCGTTGATGTAGTATGATTTCAAT 1332

Db 243 AGAGGGGTTCTTGATGTAGATGATTCGGTTCGTTGATGTAGTATGATTTCAAT 302

Qy 1333 CGTCTGAGAGCTCTATGAAATGAATGATGTAGGTAACGAATCTTCGATTTTGA 1392

Db 303 CGTCTGAGAGCTCTATGAAATGAATGATGTAGGTAACGAATCTTCGATTTTGA 362

Qy 1393 GTACCTTTGTTGAGGTAAATCAGACACCGGTATTTGCTGTGTAAAT-AAAATA 1452

Db 363 GTACCTTTGTTGAGGTAAATCAGACACCGGTATTTGCTGTGTAAAT-AAAATA 421

Qy 1453 CATTGTTGTCCTCGATTCGTGTAGTATGCTTCGATTTGAGAAAGTATCCTTG 1512

Db 422 CATTGTTGTCCTCGATTCGTGTAGTATGCTTCGATTTGAGAAAGTATCCTTG 481

Qy 1513 TTTATTCCTATTAACAATAATCAACTTTGAAAGACGGTCCGTTGATGATGA 1572

Db 482 TTTATTCCTATTAACAATAATCAACTTTGAAAGACGGTCCGTTGATGATGA 541

Qy 1573 ATGATTTGATTTTAAAGCTGTCCAAATTTCCGACGTGGCTTTTAAATACATGATCC 1632

Db 542 ATGATTTGATTTTAAAGCTGTCCAAATTTCCGACGTGGCTTTTAAATACATGATCC 601

Qy 1633 CCATACGAAATTCATGA 1650

Db 602 CCATACGAAATTCATGA 619

RESULT 5
LOCUS CK038003 585 bp mRNA linear EST 04-FEB-2005
DEFINITION 41717rbcsg_14440.y1 Oryza sativa cv. 93-11 tillering whole plant
CDNA library Oryza sativa cDNA 5', mRNA sequence.
ACCESSION CK038003
VERSION CK038003.1 GI:58609970
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 585)
AUTHORS Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
Zheng, H., Gong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
Wu, S. and Liu, J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLOS Biol. 3 (2), e38 (2005)
PUBMED 15685292
COMMENT Bioinformatics Department
Hangzhou Genomics Institute
No. 51 ZhiJiang Road, Hangzhou 310008, China
Tel: 86-571-5680586
Fax: 86-571-5680584
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 585
POLYA=No.

FEATURES
source location/Qualifiers
1..585
/organism="Oryza sativa"
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/cissue_type="whole plant"
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cDNA library"

ORIGIN
Query Match 24.2%; Score 531; DB 7; Length 585;
Best Local Similarity 98.3%; Pred. No. 7,3e-108;
Matches 569; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

Qy 1035 GCCAAGAGAGGAGACACCAAGACACGACATAGACAGAAAGCCGACCGCTTCT 1094

Db 9 GCCAAGAGAGGAGACACCAAGACACGACATAGACAGAAAGCCGACCGCTTCT 67

Qy 1095 TGATCCATATCTTCGGTGAATCTTGATCTCTTCCTCCACCTCTCTC 1154

Db 68 TGATCCATATCTTCGGTGAATCTTGATCTCTTCCTCCACCTCTCTC 127

Qy 1155 AAGGGATATG--CCCTTCGGTGTCTTGATTTATGTTCTAGGTTGTAGTACG 1211

Db 128 AAGGGATATGCTCCCTTCGGTGTCTTGATTTATGTTCTAGGTTGTAGTACG 187

Qy 1212 GGCCTGATGTAGAAAGGGATCTGTATCTGTATGATTCCTGTTCTTGATTTGGGA 1271

Db 188 GGCCTGATGTAGAAAGGGATCTGTATCTGTATGATTCCTGTTCTTGATTTGGGA 247

Qy 1272 TAGAGGGGTTCTTGATGTGATGTTATCGTTGCTGTTGATTTAGTATGTTTCAA 1331

Db 248 TAGAGGGGTTCTTGATGTGATGTTATCGTTGCTGTTGATTTAGTATGTTTCAA 307

Qy 1332 TCGTCTGAGAGCTCTATGAAATGAATGTTTGGTGGTACGATTTGCG 1391

Db 308 TCGTCTGAGAGCTCTATGAAATGAATGTTTGGTGGTACGATTTGCG 367

Qy 1392 AGTACCTTTTGTGAGGTAAATCAGACACCGGTGATTTGCTTGATTTAAAGT 1451

Db 368 AGTACCTTTTGTGAGGTAAATCAGACACCGGTGATTTGCTTGATTTAAAGT 426

Qy 1452 ACATTTGTTGTCCTCGATTCGTGTAGTATGCTTCGATTTGACGAAGCTATCTTT 1511

Db 427 ACATTTGTTGTCCTCGATTCGTGTAGTATGCTTCGATTTGACGAAGCTATCTTT 486

Qy 1512 GTTTATTCCTATTGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATTTG 1571

Db 487 GTTTATTCCTATTGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATTTG 546

Qy 1572 AATGATTTGATTTAAGCTGTCCAAATTTTCGACGCTG 1610

Db 547 AATGATTTGATTTAAGCTGTCCAAATTTTCGACGCTG 585

RESULT 6
LOCUS CF303311 578 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF1-01-016.g1 ABF1-overexpressing transgenic rice lambda phage
clone library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1-01-016, mRNA sequence.
ACCESSION CF303311
VERSION CF303311.1 GI:33675072
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 578)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

TITLE
JOURNAL
COMMENT

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

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FEATURES

source

Location/Qualifiers

1..578
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39347"
/clone="ABP1-01-016"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABP1-overexpressing transgenic rice lambda
phage cDNA library (ABP1)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-Zap XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match

24.0%; Score 526; DB 6; Length 578;

Best Local Similarity 98.3%; Pred. No. 9.6e-107;
Matches 564; Conservative 0; Mismatches 5; Indels 5; Gaps 3;

FEATURES

source

High quality sequence start: 170
High quality sequence stop: 311.
Location/Qualifiers

1..775

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:39347"
/clone="nbe0045B22r"
/issue_type="leaf"
/lab_host="E. coli DH10B"
/clone_lib="CUGI Rice BAC Library (EcoRI)"
/note="Vector: pBACindigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.
Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumuganathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 kb providing approximately 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9%. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

Query Match

21.9%; Score 479.8; DB 9; Length 775;

Best Local Similarity 90.2%; Pred. No. 2.1e-96;
Matches 564; Conservative 0; Mismatches 39; Indels 22; Gaps 4;

DB

1 AATCGAAGAGTTTCTGACCGTTTCAAGCTCACTAACAATPAGGAGCGTGCT 60
|||||

DB

689 AATCGAAGAGTTTCTGACCGTTTCAAGCTCACTAACAATPAGGAGCGTGCT 630
|||||

QY	61	AAATTTAAATAGACCTTATATATGTAAGCGGTGAATATAGAACTATATGAAGAAAATCT	120
Dp	629	AAATTTAAATAGACCTTATATATGTAAGCGGTGAATATAGAACTATATGAAGAAAATCT	570
QY	121	CATCCACCTACTTTAGTGGCAATCGGGCTAAATTAATAAAAAAGTGGCTGACACTAGTTGGT	180
Dp	569	CATCCACCTACTTTAGTGGCAATCGGGCTAAATTAATAAAAAAGTGGCTGACACTAGTTGGT	510
QY	181	TTTCTTATGTAATTAAATGAGGAAAATGAAATCATTTTGGTTAGAAATATAGGTTCAATC	240
Dp	509	TTTCTTATGTAATTAAATGAGGAAAATGAAATCATTTTGGTTAGAAATATAGGTTCAATC	450
QY	241	TCTGTCAAGAAGTTAAATTATTCGAGGTAGCCATATGTCATCAAACTCTTGAATA	300
Dp	449	TCTGTCAAGAAGTTAAATTATTCGAGGTAGCCATATGTCATCAAACTCTTGAATA	390
QY	301	AAAAAATCTTCTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTAAAAAAAAT	360
Dp	389	AAAAAATCTTCTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTAAAAAAAAT	330
QY	361	AGATGAAGATATTTCTGAACGTATCGGCAAAAGATTTAAACATATATTTATATTTAT	420
Dp	329	AGATGAAGATATTTCTGAACGTATCGGCAAAAGATTTAAACATATATTTATATTTAT	270
QY	421	AGTTTGSCATTCGTTATATGSCAGGCAATTAAGGCAATGTTACTGCA--TCTCAATT	479
Dp	269	AGTTTGSCATTCGTTATATGSCAGGCAATTAAGGCAATGTTACTCTCATTCACAAATT	210
QY	480	TTATTTAGTAATTAAAGACAATTGACTTATTTTATTTATTTATCTTTTTTCGATTAGATG	539
Dp	209	TTATTTAGTAATTAAAGACAATTGACTTATTTTATTTTATTTATCTTTTTTCGATTAGATG	165
QY	540	CAAGTACTTACGCAACAACCTTTGGCTCATGTGCATGTGTAGATGACACTCTC--ATAC	598
Dp	164	CAAGTACTTACGCAACAACCTTTGGCTCATGTGTAGATGACACTCTCTCAATAC	110
QY	599	ACGTTCAACTAGCGACACATCTCCA	623
Dp	109	CCGTTCAACTAGCGACACATCTCTA	85

RESULT 8	
AG871481	
LOCUS	AG871481 848 bp DNA linear GSS 03-NOV-2000
DEFINITION	Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence.
ACCESSION	BAC clone:X0245F03_R, genomic survey sequence.
VERSION	AG871481
KEYWORDS	AG871481.1 GI:55337716
SOURCE	GSS.
ORGANISM	Oryza sativa (indica cultivar-group)
	Oryza sativa (indica cultivar-group)
	Eurariota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
	Ehharctoidae; Oryzace; Oryza.
REFERENCE	1
AUTHORS	Katagiri,S., Wu,J., Ito,Y., Karasawa,W., Shibata,M., Kanamori,H., Katayose,Y., Namki,N., Matsumoto,T. and Sasaki,T.
TITLE	End Sequencing and Chromosomal in silico Mapping of BAC Clones Derived from an indica Rice Cultivar, Kasalath
JOURNAL	Breeding Science 54, 273-279 (2004)
REFERENCE	2 (bases 1 to 848)
AUTHORS	Sasaki,T., Matsumoto,T. and Wu,J.
TITLE	Direct Submissions
JOURNAL	Submitted (23-OCT-2004) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki, 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT	The orientation of the sequence is from SP6 side of the BAC clone.
FEATURES	Location/Qualifiers
SOURCE	1..848

[illegible]

RESULT 9	
CF305170	
LOCUS	324 bp mRNA linear EST 15-AUG-2003
DEFINITION	ABR1--06-P15.g1 ABR3-overexpressing transgenic rice lambda phage
ACCESSION	CDNA library (ABR1) Oryza sativa [japonica cultivar-group] CDNA
VERSION	clone ABR1--06-P15, mRNA sequence.
KEYWORDS	CF305170
SOURCE	CF305170.1 GI:33676931
ORGANISM	EST.
	Oryza sativa [japonica cultivar-group]
	Oryza sativa [japonica cultivar-group]
	Eubaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
	Spermatophytes, Magnoliophyta, Liliopsida, Poales, Poaceae;
	Erihartoideae; Oryzaceae; Oryza.
REFERENCE	1 (bases 1 to 324)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
	Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
	Large-scale Sequencing Analysis of Rice ESTs
TITLE	Unpublished (2003)
JOURNAL	Contact: Nahm B.H.
COMMENT	Genomics and Genetics Institute, Greengene Biotech Inc.; Division
	of Bioscience and Bioinformatics, Myongji University
	Yongin, Kyeonggi, Korea
	Tel: 82 31 330 6193
	Fax: 82 31 321 6355
	Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
FEATURES	Location/Qualifiers
source	1..324
	/organism="Oryza sativa [japonica cultivar-group]"
	/mol_type="mRNA"
	/cultivar="Nackdong"
	/db_xref="taxon:39947"
	/clone="ABR1--06-P15"
	/rissue_type="leaf"
	/dev_stage="14 days after germination"

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/lab_host="E.coli SOLR"
/clone.lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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ORIGIN

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Query Match      13.0%; Score 286.2; DB 6; Length 324;
Best Local Similarity 97.8%; Pred. No. 4.1e-53;
Matches 312; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

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QY 1046 GGAGGACCAAGACAGCGACGCTAGCAGACCGGACCGCCTTCTTCATCCATAT 1105
DB 7 GGAGGACCAAGACAGCGACGCTAGCAGACCGGACCGCCTTCTTCATCCATAT 65
QY 1106 CTTCCGTCGAGTTCTTGGTCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 1165
DB 66 CTTCCGTCGAGTTCTTGGTCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 125
QY 1166 G---CCCTTCGCTGTTCTTGAATTATTTCTAGTGTGTAGTACGGGCGTTGATGT 1222
DB 126 GCCTCCCTTCGCTGTTCTTGAATTATTTCTAGTGTGTAGTACGGGCGTTGATGT 185
QY 1223 TAGGAAAGGGAGTCGTATCTGTGATGATTCCTCTCTGATTTGGATAGAGGGGTTTC 1282
DB 186 TAGGAAAGGGAGTCGTATCTGTGATGATTCCTCTCTGATTTGGATAGAGGGGTTTC 245
QY 1283 TTGATGTCATGATGATCGGTTCCGTTTGTATGATGATGATGATGATGATGATGATGAT 1342
DB 246 TTGATGTCATGATGATCGGTTCCGTTTGTATGATGATGATGATGATGATGATGATGAT 305
QY 1343 GCTCTATGGAATGAATG 1361
DB 306 GCTCTATGGAATGAATG 324

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RESULT 10      288 bp      mRNA      linear      EST 15-FEB-2003
LOCUS      CF304743
DEFINITION      ABF1--05-N05-g1 ABF3-overexpressing transgenic rice lambda phage
                  cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
                  clone ABF1--05-N05, mRNA sequence.
ACCESSION      CF304743
VERSION        CF304743.1 GI:33676504
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Oryza sativa (japonica cultivar-group)
REFERENCE      1 (bases 1 to 288)
AUTHORS        Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, Greengene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
                Location/Qualifiers
FEATURES
SOURCE         1..288
                /organism="Oryza sativa (japonica cultivar-group)"
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                /cultivar="Nackdong"
                /db_xref="taxon:39947"
                /clone="ABF1-05-N05"

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/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone.lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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ORIGIN

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Query Match      11.3%; Score 248.6; DB 6; Length 288;
Best Local Similarity 97.2%; Pred. No. 1.1e-44;
Matches 275; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

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QY 1046 GGAGGACCAAGACAGCGACGCTAGCAGACCGGACCGCCTTCTTCATCCATAT 1105
DB 7 GGAGGACCAAGACAGCGACGCTAGCAGACCGGACCGCCTTCTTCATCCATAT 65
QY 1106 CTTCCGTCGAGTTCTTGGTCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 1165
DB 66 CTTCCGTCGAGTTCTTGGTCGATCTCTCCCTCCACCTCTCTCAGAGGTATGT 125
QY 1166 G---CCCTTCGCTGTTCTTGAATTATTTCTAGTGTGTAGTACGGGCGTTGATGT 1222
DB 126 GCCTCCCTTCGCTGTTCTTGAATTATTTCTAGTGTGTAGTACGGGCGTTGATGT 185
QY 1223 TAGGAAAGGGAGTCGTATCTGTGATGATTCCTCTCTGATTTGGATAGAGGGGTTTC 1282
DB 186 TAGGAAAGGGAGTCGTATCTGTGATGATTCCTCTCTGATTTGGATAGAGGGGTTTC 245
QY 1283 TTGATGTCATGATGATCGGTTCCGTTTGTATGATGATGATGATGATGATGATGATGAT 1325
DB 246 TTGATGTCATGATGATCGGTTCCGTTTGTATGATGATGATGATGATGATGATGATGAT 288

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RESULT 11      239 bp      mRNA      linear      EST 05-FEB-2005
LOCUS      CK042297
DEFINITION      43579riceh_11658.y1 Oryza sativa cv. P646 panicle fertile cDNA
                  library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
                  sequence.
ACCESSION      CK042297
VERSION        CK042297.1 GI:58653617
KEYWORDS       EST.
SOURCE         Oryza sativa (indica cultivar-group)
ORGANISM       Oryza sativa (indica cultivar-group)
REFERENCE      1 (bases 1 to 239)
AUTHORS        Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
                Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
                Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
                Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
                Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
                Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
                Wu,S. and Liu,J.
TITLE          The Genomes of Oryza sativa: A History of Duplications
JOURNAL        Plos Biol. 3 (2), e38 (2005)
COMMENT        PUBMED 15685292
                Contact: Yan Zhou
                Bioinformatics Department
                Hangzhou Genomics Institute
                No.51 Zhijiang Road, Hangzhou 310008, China
                Tel: 86-571-56805886
                Fax: 86-571-56805884
                Email: zhouyan@genomics.org.cn
                Seq primer: M13 Forward
                High quality sequence stop: 239
                POLYA=No.

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QY 1109 CCGGTGAGTCTTGGTCGATCTCTCCCTCCACCTCTCTCCACAGGGTAT 1163
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DB 182 CCGGTGAGTCTTGGTCGATCTCTCCCTCCACCTCTCTCCACAGGGTCT 236

RESULT 14
CF278393 479 bp mRNA linear EST 14-AUG-2003
LOCUS CF278393
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14FTL-04-E15,
mRNA sequence.
ACCESSION CF278393.1 GI:33655779
VERSION CF278393
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 479)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers
1..479
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14FTL-04-E15"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1lb="Rice etiolated leaf plasmid cDNA library
(14FTL)"
/note="Vector: PCR4-TOPO; Site 1: BcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match 8.3%; Score 181.4; DB 6; Length 479;
Best Local Similarity 94.3%; Pred. No. 1.2e-29;
Matches 199; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

QY 953 AGGCAAGAAAACAAGCATCTCTCTCCATCTATAATCTCCCTCTTTCCTCC 1012
|||
DB 50 AGAAAAAAATTCAGCATCTCTCTCCCTGATATAATCTCTCCCTCTTTCCTCC 109
|||
QY 1013 TCTCTATATAGAGGATCTCAAGCCAGAGAGGAGAGACCAAGAGACACGGGATTAC 1072
|||
DB 110 TCTCTATATAGAGGATCTCAAGCCAGAGAGGAGAGACCAAGAGACACGGGATTAC 169
|||
QY 1073 AGAAGCCGAGGACCGCTCTTTCATCATATCTCCGATGAGTTCTTGGGATCTC 1132
|||
DB 170 AGAAGCCGAGGACCGCTCTTTCATCATATCTCCGATGAGTTCTTGGGATCTC 228
|||
QY 1133 TTCCCTCTCCACCTCTCTCTCAAGGGTAT 1163
|||
DB 229 TTCCCTCTCCACCTCTCTCTCAAGGGTCT 259
|||

RESULT 15
CB214615 571 bp mRNA linear EST 05-FEB-2003

DEFINITION OML04895 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',
mRNA sequence.
ACCESSION CB214615
VERSION CB214615.1 GI:28260706
KEYWORDS EST.
SOURCE Oryza minuta
ORGANISM Oryza minuta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 571)
AUTHORS Shin,J.S.
TITLE Oryza minuta HybridZAP-2.1 XR library
JOURNAL Unpublished (2003)
COMMENT Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 920 3430
Fax: 00 82 2 927 9028
Email: jshin@kucn.korea.ac.kr.

FEATURES
source location/Qualifiers
1..571
/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
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ORIGIN
Query Match 8.3%; Score 181.4; DB 6; Length 571;
Best Local Similarity 69.7%; Pred. No. 1.2e-29;
Matches 381; Conservative 0; Mismatches 116; Indels 50; Gaps 8;

QY 1071 GCAGAGCCGAGCAGACCGCTCTTTCATCATATCTCCGATGAGTTCTTGGTATC 1130
|||
DB 10 GCAGTACGCGAGCAGACCGCTCTTTCATCATATCTCCGATGAGTTCTTGGTATC 68
|||
QY 1131 TCTTCCCTCTCCACCTCTCTCC-----TCACAGGATATGCGCTTGGTCTTGG 1183
|||
DB 69 TCTTCCCTCTCTCCACCTCTCTCCAGGATATGTTGCGTCTCTTCTTCCCTCTT 128
|||
QY 1184 GATTATATGTTCTAGATTGTGTAGTACGAGCGCTGATGTTAGAAAGGAGATCTGATCT 1243
|||
DB 129 CTGGAATCTGTGTAGATTGTGTAGTGTGTGCTTATATGTTAGA-----GGTT 176
|||
QY 1244 GTGATGATCTCTGTTCTTGGATTTGGATAGAGGGGTTCTTGGATGATGATTCGGT 1303
|||
DB 177 TTTCTCAAGAGGAGATCTGATATTTGATAGAGTATGTTCTTGTGATGTTA----- 231
|||
QY 1304 TCGGTTGATTTAGTATGATGTTTTCATCTCTCTGAGAGCTCTATAGAAAGAAATGCT 1363
|||
DB 232 -----AATTTGATCTGTTGGAAATCTGTGAGAGCTATAGAGGAAATG----- 275
|||
QY 1364 TTAGGATACGGAATCTGCGATTTTGTGAGTACCTTTTGTGAGTAAATCAGAGCAC 1423
|||
DB 276 TTAGGATACGGAATTTTGGATTTTCTGAGTACATTGATTTGAGGTTAAATCAGAGCAC 335
|||
QY 1424 CCGTATTTTGGCTTGTGATTAATAAGTACATTTTGGTCTCTGATTTCTGATGAT 1483
|||
DB 336 TGGATATTTTGGCTTGTGATTAATAA--TACGGTTTGTGCTCTGATTTCTGATGAT 394
|||
QY 1484 GCTTTCGATTTGAGAGACCTATCTTTGTTTATCTCCATTTGAACAATAATCCAAC 1543
|||
DB 395 GCTGTCGATTTGAGAGACCTATCTCTTTGTTTATCTCCATTTGAACAATAATCCAAC 453
|||
QY 1544 TTGGAAGACGTCCTGATGATG-----AGATTAATGATTTGATTTTAAAGCTGTCCA 1596
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DB 454 TTGGAAGACGTCCTGATGATGATGCTACTCGCGTTACATGATGATTTCTTAAGTCTGTCT 513
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QY 1597 AATTTTC 1603
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Db 514 AAATTTC 520

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Job time : 7880 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd

OM nucleic - nucleic search, using sw model

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(without alignments)
9447.331 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	867.2	39.5	898	3	US-10-012-070A-50	Sequence 50, Apple
2	56.8	2.6	7218	3	US-08-232-463-13	Sequence 150, Apple
3	55.2	2.5	612	3	US-09-902-540-1357	Sequence 1357, Apple
4	55.2	2.5	601	3	US-09-949-016-196365	Sequence 196365, Apple
5	53.8	2.5	601	3	US-09-949-016-196366	Sequence 196366, Apple
6	53.8	2.5	601	3	US-09-949-016-196367	Sequence 196367, Apple
7	53.8	2.5	451924	3	US-09-949-016-128986	Sequence 128986, Apple
8	53.8	2.5	451925	3	US-09-949-016-17305	Sequence 17305, Apple
9	53.6	2.4	700	3	US-09-735-871-1038	Sequence 1038, Apple
10	53.6	2.4	11413	3	US-09-969-0708-22	Sequence 22, Apple
11	52.8	2.4	16573	3	US-09-949-016-14876	Sequence 14876, Apple
12	51.2	2.3	998	3	US-09-122-400A-5	Sequence 5, Apple11
13	51	2.3	95255	3	US-09-949-016-17067	Sequence 17067, Apple
14	50.2	2.3	50000	3	US-09-662-254B-24	Sequence 24, Apple
15	49.8	2.3	601	3	US-09-949-016-30531	Sequence 30531, Apple
16	49.8	2.3	601	3	US-09-949-016-37150	Sequence 37150, Apple
17	49.8	2.3	601	3	US-09-949-016-37164	Sequence 37164, Apple
18	49.8	2.3	601	3	US-09-949-016-145868	Sequence 145868, Apple
19	49.8	2.3	601	3	US-09-949-016-146136	Sequence 146136, Apple
20	49.8	2.3	601	3	US-09-949-016-146404	Sequence 146404, Apple
21	49.8	2.3	205044	3	US-09-949-016-15851	Sequence 15851, Apple
22	49.8	2.3	205044	3	US-09-949-016-15852	Sequence 15852, Apple
23	49.8	2.3	205044	3	US-09-949-016-15853	Sequence 15853, Apple
24	49.8	2.3	223471	3	US-09-949-016-12387	Sequence 12387, Apple

ALIGNMENTS

C	25	49.8	2.3	223471	3	US-09-949-016-13724	A	Sequence 12724, A
C	26	49.8	2.3	223471	3	US-09-949-016-13725	A	Sequence 12725, A
C	27	49.8	2.3	223471	3	US-09-949-016-13725	A	Sequence 12725, A
C	28	49.8	2.2	5526	3	US-08-751-359-21	App	Sequence 21, App
C	29	48.4	2.2	5526	3	US-08-907-146-21	App	Sequence 21, App
C	30	48.4	2.2	6152	3	US-08-973-462-1	App	Sequence 1, App
C	31	48.4	2.2	87644	3	US-09-949-016-16041	A	Sequence 16041, A
C	32	48.2	2.2	601	3	US-09-949-016-30532	A	Sequence 30532, A
C	33	48.2	2.2	601	3	US-09-949-016-37151	A	Sequence 37151, A
C	34	48.2	2.2	601	3	US-09-949-016-37165	A	Sequence 37165, A
C	35	48.2	2.2	601	3	US-09-949-016-145869	A	Sequence 145869, A
C	36	48.2	2.2	601	3	US-09-949-016-161337	A	Sequence 161337, A
C	37	48.2	2.2	731	2	US-09-949-016-16405	A	Sequence 164405, A
C	38	48.2	2.2	105001	3	US-08-451-405A-2	App	Sequence 2, App
C	39	48.2	2.2	105002	3	US-09-949-002-627	App	Sequence 627, App
C	40	48.2	2.2	251572	3	US-09-949-002-821	App	Sequence 821, App
C	41	48	2.2	251582	3	US-09-949-016-117296	App	Sequence 17996, App
C	42	47.8	2.2	1341	3	US-09-949-016-11973	A	Sequence 11973, A
C	43	47.8	2.2	1410	3	US-09-830-230A-571	App	Sequence 571, App
C	44	47.6	2.2	212449	3	US-09-949-016-15419	App	Sequence 15419, App
C	45	47.4	2.2	20674	3	US-09-641-638-651	App	Sequence 651, App

```

RESULT 1
US-10-012-070A-50
; Sequence 50, Application US/10012070A
; Patent No. 6867293
; GENERAL INFORMATION:
; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Andrews, Christopher
; APPLICANT: Bachoo, Satvinder
; APPLICANT: Pickerill, Andrew
; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/GS00/01573
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patencent Ver. 2.0
; SEQ ID NO 50
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Oryza sp.
US-10-012-070A-50

Query Match      39.5%; Score 867.2; DB 3; Length 898;
Best Local Similarity 99.2%; Pred. No. 6,7e+201;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2

QY      1 AATCGGAAAGTTTCGTGACCGTTTTTACGCTCTTAACAATAATATAGGAACGTGTGCT    60
DB      2 AATCGGAAAGTTTCGTGACCGTTTTTACGCTCTTAACAATAATATAGGAACGTGTGCT    61

QY      61 AAATATAAATGAGACCTTATATATATATATAGCGCTGATATACTAGAACATATAGAAAAAAT    120
DB      62 AAATATAAATGAGACCTTATATATATATATATAGCGCTGATATACTAGAACATATAGAAAAAAT    121

QY      121 CATCACCCTATTATAGTGCGCAATCGGGCTTAAAATAAAAAGAATCGGTACATCATAGTTTGGT    180
DB      122 CATCACCCTATTATAGTGCGCAATCGGGCTTAAAATAAAAAGAATCGGTACATCATAGTTTGGT    181

QY      181 TTTCTTAGTATATAGTGGAAGAAATGAATCATTTATTTGCTTAGAATATATCGTTCACATC    240
DB      182 TTTCTTAGTATATAGTGGAAGAAATGAATCATTTATTTGCTTAGAATATATAGTTCACATC    241

QY      241 TCTGTGATGAAGTAAATTTATTCAGGTAGCCATATTTGTATCAAATCTTTCTTGGAATA    300
DB      242 TCTGTGATGAAGTAAATTTATTCAGGTAGCCATATTTGTATCAAATCTTTCTTGGAATA    301

```

QY 301 AAAAAATCTTCTAGCTGAACCTCAATGCGTAAAGAGATATTTTTTAAAAAAAT 360
Db 302 AAAAAATCTTCTAGCTGAACCTCAATGCGTAAAGAGATATTTTTT---AAAAAAT 358
QY 361 AAAAAATCTTCTAGCTGAACCTCAATGCGTAAAGAGATATTTTTTAAAAAAAT 420
Db 359 AAAAAATCTTCTAGCTGAACCTCAATGCGTAAAGAGATATTTTTTAAAAAAAT 418
QY 421 AGTTGTGCAATTCGTTATATGCAAGCTCAATTAAGAGATGCTTACATCTCAATTT 480
Db 419 AGTTGTGCAATTCGTTATATGCAAGCTCAATTAAGAGATGCTTACATCTCAATTT 478
QY 481 TATTTAGTATTAAGACAATGACTTATTTTATTTATTTATTTTTCGATTAGATGC 540
Db 479 TATTTAGTATTAAGACAATGACTTATTTTATTTATTTATTTTTCGATTAGATGC 538
QY 541 AAGGTAATTAAGACAATGACTTATTTTATTTATTTTATTTTTCGATTAGATGC 599
Db 539 AAGGTAATTAAGACAATGACTTATTTTATTTATTTTATTTTTCGATTAGATGC 598
QY 600 CGTTCACTAGGCAACATCTCAATATGACTCGCTTATTAATTAATTAATTAATTAAT 659
Db 599 CGTTCACTAGGCAACATCTCAATATGACTCGCTTATTAATTAATTAATTAATTAAT 658
QY 660 ATCTGAATTCAGCACTTCACATCAACAGACCACTTTTATTAATTAATTAATTAAT 719
Db 659 ATCTGAATTCAGCACTTCACATCAACAGACCACTTTTATTAATTAATTAATTAAT 718
QY 720 AATTAATTTTACAGATAGCAATGAAAGTATGAAAGCAATTTTATTTTACATTA 779
Db 719 AATTAATTTTACAGATAGCAATGAAAGTATGAAAGCAATTTTATTTTACATTA 778
QY 780 AAAAAAAGAAATTTTGTCTGCGCGAGCGCAATCTCCATATTTGGGCAACAGCA 839
Db 779 AAAAAAAGAAATTTTGTCTGCGCGAGCGCAATCTCCATATTTGGGCAACAGCA 838
QY 840 ACAACAGAGTGGCTGCCACAGAACCCACAAAAAACGATGATTAACGAGAGACAC 899
Db 839 ACAACAGAGTGGCTGCCACAGAACCCACAAAAAACGATGATTAACGAGAGACAC 898

RESULT 2

US-08-232-463-14
Sequence 14, Application US/08232463
GENERAL INFORMATION:
PATENT No. 5670367
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZpC-Fls
US-08-232-463-14

Query Match 2.6%, Score 56.8; DB 2; Length 7218;
Best Local Similarity 6.6%, Pred. No. 0.0011;
Matches 28; Conservative 221; Mismatches 173; Indels 0; Gaps 0;

QY 1680 TTCCCTGTTCTCCGATTTGCTTAGTCCAGAAATTTTTCCTCAATATCTTAAAAAG 1739
Db 1069 YY 1128
QY 1740 TCACCTTTCGTGTCAGTCAATGAATGATGCTACAAATATGCTTTATAGCTTATC 1799
Db 1129 YY 1188
QY 1800 CTAGCTGATGTCAGTTATAGTAATACCCCTATAGTTTGTGACGAGAAAGAACTATC 1859
Db 1189 YY 1248
QY 1860 CGATTCGTGATCTCATTTTATTAATTAATGAATGAATGATGATGAAGATATTCAT 1919
Db 1249 YY 1308
QY 1920 TGATTAATTTTATTAATAGCTTTCACCCCTCATTTATCTGAGCTGAAGCTGGCATG 1979
Db 1309 YY 1368
QY 1980 AACTGCTCATTTTGTTCCTCAATTCACATCATATCATATCATATCATCTCTGAT 2039
Db 1369 YY 1428
QY 2040 CTACCTGAGAAAGTTCTTTTGTGTTATTCCTGACTGCTGATTAACAGAAAGAAATTA 2099
Db 1429 YYYYYYGCACAAATCTTCTATCTCTTAACTACTGATGATAGTAAATTAACAGTGA 1488
QY 2100 TG 2101
Db 1489 TG 1490

RESULT 3

US-09-902-540-1357/C
Sequence 1357, Application US/09902540
GENERAL INFORMATION:
PATENT No. 6833447
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(11549)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16625
SEQ ID NO 1357
LENGTH: 612

TYPE: DNA
ORGANISM: Myxococcus xanthus
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(612)
OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

Query Match 2.5%; Score 55.2; DB 3; Length 612;
Best Local Similarity 44.2%; Pred. No. 0.0012;
Matches 222; Conservative 0; Mismatches 280; Indels 0; Gaps 0;

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QY 1680 TTCCTGCTTCCTCCAGATTCCTTAGTCCAGAAATTTTCCCAATATCTTAAAAAG 1739
DB TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 449
QY 1740 TCACCTTCGCTTCAGTCAATGAATGATGCTACAAATAGCTTTATAGCTTATC 1799
DB 448 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 389
QY 1800 CTAGCTGATGCTCAGTTTATAGTAATACCCGATAGTTAGTCAGAGAGAACTATC 1859
DB 388 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 329
QY 1860 CCAATTCGATCTCCATTTTATATATGAATGAAGTGAAGTGAAGTGAAGTGAAGT 1919
DB 328 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 269
QY 1920 TGAATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 1979
DB 268 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 209
QY 1980 AACTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 2039
DB 208 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 149
QY 2040 CTACCTGTAAGATTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 2099
DB 148 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 89
QY 2100 TGAAGCTGTAATCGGATAGTAACTGCTTCCTTCCTTCCTTCCTTCCTTCCT 2159
DB 88 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 29
QY 2160 TCTTGCTGAGCTTGCCACTT 2181
DB 28 TTTTTCCTGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 7
```

RESULT 4
US-09-949-016-196365/C
Sequence 196365, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 196365
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-196365

Query Match 2.5%; Score 53.8; DB 3; Length 601;
Best Local Similarity 53.0%; Pred. No. 0.0026;
Matches 115; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

```
QY 319 AACTCAATGGGTAAGAGATATTTTAAAAAATAGATAGATATTCGA 378
DB 298 AATTAAATATATATATATATATATATATATATATATATATATATATATATAT 239
QY 379 ACGTATCGGCAAGATTAACATATATATATATATATATATATATATATATATAT 438
DB 238 AATTAATATATATATATATATATATATATATATATATATATATATATATATAT 179
QY 439 ATCGACGCTATTAAGACATGCTTACTCCATCTCAATTTTATAGTAATTAAGAC 498
DB 178 AATTAAATATATATATATATATATATATATATATATATATATATATATATAT 119
QY 499 AATTGACTTATTTTATATATATATATATATATATATATATATATATATATAT 535
DB 118 AATTAAATATATATATATATATATATATATATATATATATATATATATATAT 82
```

RESULT 5
US-09-949-016-196366/C
Sequence 196366, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 196366
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-196366

Query Match 2.5%; Score 53.8; DB 3; Length 601;
Best Local Similarity 53.0%; Pred. No. 0.0026;
Matches 115; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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QY 319 AACTCAATGGGTAAGAGATATTTTAAAAAATAGATAGATATTCGA 378
DB 298 AATTAAATATATATATATATATATATATATATATATATATATATATATATAT 237
QY 379 ACGTATCGGCAAGATTAACATATATATATATATATATATATATATATATATAT 438
DB 236 AATTAATATATATATATATATATATATATATATATATATATATATATATATAT 177
QY 439 ATCGACGCTATTAAGACATGCTTACTCCATCTCAATTTTATAGTAATTAAGAC 498
DB 176 AATTAAATATATATATATATATATATATATATATATATATATATATATATAT 117
QY 499 AATTGACTTATTTTATATATATATATATATATATATATATATATATATATAT 535
DB 116 AATTAAATATATATATATATATATATATATATATATATATATATATATATAT 80
```

RESULT 6
US-09-949-016-196367/C
Sequence 196367, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:


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1 CURRENT FILING DATE: 2000-12-11
2 PRIOR APPLICATION NUMBER: US 60/170,257
3 PRIOR FILING DATE: 1999-12-10
4 PRIOR APPLICATION NUMBER: US 60/196,046
5 PRIOR FILING DATE: 2000-04-10
6 NUMBER OF SEQ ID NOS: 2058
7 SOFTWARE: FASTSEQ for Windows Version 4.0
8 SEQ ID NO 1038
9 LENGTH: 700
10 TYPE: DNA
11 ORGANISM: Homo sapiens
12 FEATURE:
13 NAME/KEY: misc_feature
14 LOCATION: (1) ... (700)
15 OTHER INFORMATION: n = A,T,C or G
16 US-09-735-271-1038

```

Query Match	2.4%	Score 53.6	DB 3	Length 700
Best Local Similarity	45.8%	Pred. No. 0.003		
Matches 220, Conservative	0	Mismatches 259	Indels 1	Gaps 1

[illegible]

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RESULT 10
US-09-806-708B-22
Sequence 22. Application US/09806708B
Patent No. 678342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:

```

```

; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., J.a., and B.n. PstI promoters
US-09-806-708B-22

```

Query Match 2.4%; Score 53.6; DB 3; Length 1141;
 Best Local Similarity 8.4%; Pred. No. 0.0036;
 Matches 57; Conservative 290; Mismatches 330; Indels 1; Gaps 1

[illegible]

```

, RESULT 11
, US-09-949-016-14876
, Sequence 14876, Application US/09949016
, Patent No. 6812339
, GENERAL INFORMATION:
, APPLICANT: VENTER, J. Craig et al.
, TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
, TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
, FILE REFERENCE: C1001307
, CURRENT APPLICATION NUMBER: US/09/949, 016
, CURRENT FILING DATE: 2000-04-14
, PRIOR APPLICATION NUMBER: 60/241,755
, PRIOR FILING DATE: 2000-10-20
, PRIOR APPLICATION NUMBER: 60/237,768
, PRIOR FILING DATE: 2000-10-03
,

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QY 541 AAGTACTTACGACACACTTTGCTCATGTCATGTCGATGCACTCTCTATACAC 600
DB 42318 AATATATATATATATATATATATATATATATATATATATATATATATAT 42377
QY 601 GTTCACTGCGACACATCTCCAAATATCACTGCGCTATTATTAATACATTTAGTAGCAATA 660
DB 42378 ATATTTATATATATATATATATATATATATATATATATATATATATATATAT 42437
QY 661 TCTGAATTCAGACACTTCACATCAGACACACTTTTATATATATCTTAAATACAAAA 720
DB 42438 TATTAATATAT--AATTAATTAATATATATATATATATATATATATATATATAT 42495
QY 721 ATATATTTACAGATATGATGAAAGATGAAAGCACTATTTAGCTTTTCATACAA 780
DB 42496 ATATATTTACAGATATATATATATATATATATATATATATATATATATATATAT 42555
QY 781 AAAAAAAA 789
DB 42556 TATTAATATA 42564

RESULT 14
US-09-662-254B-24/C
; Sequence 24, Application US/09662254B
; Patent No. 6933145
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Li, Yi
; APPLICANT: Bawden, Alison Louise
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; FILE REFERENCE: UF-221C1X1
; CURRENT APPLICATION NUMBER: US/09/662,254B
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Amsacta moorei entomopoxvirus
US-09-662-254B-24

Query Match 2.3%; Score 50.2; DB 3; Length 50000;
Best Local Similarity 46.0%; Pred. No. 0.084;
Matches 169; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

QY 175 TTTCGTTTCTAGTAATTAAGTGGAAATGAATTCATTTGCTTGAATATACGTT 234
DB 44081 TTTTATTTATTAATTAATTTTGTATCATCTAATACATTAATTCGATCATTATATGA 44022
QY 235 CACATCTGTCATGAGTAAATTAATTCAGGTACCAATTCATCACTCTCTC 294
DB 44021 TTTTTCATCATGAATGAATTAATTAATTAACATTAATATATATATATATATAT 43962
QY 295 TGAATTAATAAATCTTTCTAGCTGAATCTCAATGGGTAAAGAGATATTTTTTAAAA 354
DB 43961 TAAATTAATAAATGATATATCTTTTAAATATATAGCAAAATATAGTTTATTTTCAAT 43902
QY 355 AAAAAATGAATGAATATTCGAAGTATCGGCAAAAGTTTAAACATTAATTAATATA 414
DB 43901 TGGTGAATTAATAAATTAAGATTAATGAATAATGAATTAATAAATTAATTAATAT 43842
QY 415 TTTTATAGTTTGCATTCGTTATATCGACATTAATGAAGATCTTACTCATCTC 474
DB 43841 AAAAAATGTTATATTAATGATGATATGAAATTAACATTAATTAATTAATATATTC 43782
QY 475 AATTTTATTTAGTAATTAAGAACAATGACTATTTTATTTATTTATCTTTTTCGATT 534
DB 43781 ATATTAATTAATTAATTAATTAATAAATTAATAATTTTATTAATTAATCTGATGAAAA 43722
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QY 535 AGATGCA 541
DB 43721 ACATTCGA 43715

RESULT 15
US-09-949-016-30531/C
; Sequence 30531, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30531
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-30531

Query Match 2.3%; Score 49.8; DB 3; Length 601;
Best Local Similarity 46.0%; Pred. No. 0.024;
Matches 168; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 51 AACGTGTCTAATTAATTAATGAGACTTATATATAGCGCTGATTAAGACTATGCT 110
DB 434 AATATATTAATAAATATTTATATATATTTTAAATTAATAATTAATTAATTAATATAT 375
QY 111 AAAAAAACTCACTCACTCTTTAGTGGCAATCGGCTAATTAATAAAGAGTCTACA 170
DB 374 ATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 315
QY 171 CTAGTTTCGTTTCTTCTAGTAATTAAGTGGAAAAATGAATCATTTGCTTGAATATA 230
DB 314 ATATTTATATATATTTTAAATTAATAATTAATAAATATATATATATTTTAAATATA 255
QY 231 CGTTCATCTCTGTCATGAAGTTAATTTATTCAGGTAGCCATTAATGTCATCAACTC 290
DB 254 AATATTAATAAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTTTAAATA 195
QY 291 TTCTGAATTAATAAATCTTTCTAGCTGAATCAATGGGTAAAGAGATATTTTTTTT 350
DB 194 TAAATTAATTAATAAATTAATTAATTTTAAATTAATAATTAATAAATTAATTAATTTTAAA 135
QY 351 AAAAAAAATGAATGAATATTCGAAGTATCGGCAAAAGTTTAAACATTAATATAT 410
DB 134 TATTAATTAATTAATAATTAATTAATTTTAAATTAATAATTAATAAATTAATTAATTTTA 75
QY 411 ATPAT 415
DB 74 AATPAT 70

Search completed: April 21, 2006, 09:00:41
Job time : 415 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:44 ; Search time 10738 Seconds

(without alignments)
11619.610 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195
Sequence: 1 aatccgaaagtcttcgcac.....cacttcaccagcaagttc 2195

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank! :
1: gb_ba : *
2: gb_in : *
3: gb_env : *
4: gb_om : *
5: gb_ov : *
6: gb_pat : *
7: gb_ph : *
8: gb_pr : *
9: gb_ro : *
10: gb_str : *
11: gb_sy : *
12: gb_un : *
13: gb_vl : *
14: gb_hcg : *
15: gb_pl : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	100.0	2195	6	CQ876145
2	2141.4	97.6	3192	15	OSGOS92G
3	2139.2	97.5	3032	6	CQ895917
4	2133.4	97.2	9361	6	BD251965
5	2133.4	97.2	10629	6	BD251965
6	2131.6	97.1	105692	14	AP003953
7	2131.6	97.1	110000	15	AP008213_206
8	2131.6	97.1	144741	15	AP004674
9	2128.4	97.0	14203	11	AF294979
10	2128.4	97.0	14230	11	AF294980
11	2115.2	96.4	2191	6	CS055056
12	867.2	39.5	898	6	AR643981
13	867.2	39.5	898	6	AX044095
14	867.2	39.5	898	6	AX044183
15	124.2	5.7	752	15	AK120697
16	108.2	4.9	744	15	AF094774
17	94.6	4.3	1275	15	AK105037
18	85.8	3.9	110000	15	AP008211_062

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C	20	85.8	3.9	143966	15	AC135920	AC135920 Oryza sat
C	21	85.8	3.9	172647	15	AC130732	AC130732 Oryza sat
C	22	84.6	3.9	110000	15	AP008209_328	Continuation (329
C	23	84.6	3.9	162497	15	AC090871	AC090871 Oryza sat
C	24	79.8	3.6	110000	15	AP008214_178	Continuation (179
C	25	79.8	3.6	110000	15	AP008213_289	Continuation (290
C	26	79.8	3.6	146856	15	AP004675	AP004675 Oryza sat
C	27	79.8	3.6	180015	15	AP005167	AP005167 Oryza sat
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C	30	75	3.4	161676	15	AC135907	AC135907 Genomic s
C	31	72.4	3.3	110000	15	AP008213_199	Continuation (200
C	32	72.4	3.3	158880	15	AP005103	AP005103 Oryza sat
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C	39	69.6	3.2	110000	15	AP008208_197	Continuation (198
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C	42	69.4	3.2	110000	15	AP008217_054	Continuation (55 o
C	43	69.4	3.2	142241	15	AC123523	AC123523 Oryza sat
C	44	69.4	3.2	339485	15	AF172282	AF172282 Oryza sat
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ALIGNMENTS

RESULT 1	CQ876145	2195 bp	DNA	linear	PAT 04-OCT-2004
LOCUS	CQ876145	Sequence 1 from Patent WO2004065596.			
DEFINITION	CQ876145				
ACCESSION	CQ876145				
VERSION	CQ876145.1	GI:53789748			
KEYWORDS					
SOURCE					
ORGANISM	Oryza sativa				
	Oryza sativa				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Ehrhartoideae; Oryzaceae; Oryza.				
REFERENCE	1	Hatzfeld, Y. and Inze, D.			
AUTHORS					
TITLE	Regulatory Sequence				
JOURNAL	Patent: WO 2004065596-A 1 05-AUG-2004;				
	CropDesign N.V. (BE)				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:4530"				
ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 2195;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	AATCGAAGAGTTTCGACCGTTTTCAGCTCTTAACAATATAGGAAGTGTCT	60		
DB	1	AATCGAAGAGTTTCGACCGTTTTCAGCTCTTAACAATATAGGAAGTGTCT	60		
QY	61	AAATATTAATGAGACTTATATATGAGCGCTGATTAAGTAAGTAAGAAACT	120		
DB	61	AAATATTAATGAGACTTATATATGAGCGCTGATTAAGTAAGTAAGAAACT	120		
QY	121	CATCACTACTCTTATGTCGCAATCGGCGCTTAATATATATATATATATAT	180		
DB	121	CATCACTACTCTTATGTCGCAATCGGCGCTTAATATATATATATATATAT	180		
QY	181	TTTCCTTAGTATTAATGAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG	240		
DB	181	TTTCCTTAGTATTAATGAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG	240		

Db 181 TTTCCCTAGTAATTAAGTGGGAAATGAATCATTTGCTTGAATATATACCTGCATC 240
 Qy 241 TCTGTCAGTAAGTTAAATTAATCGAGTGGCCATATTTGCATCAAACTCTTGAATA 300
 Db 241 TCTGTCATAGTAAGTTAAATTAATCGAGTGGCCATATTTGCATCAAACTCTTGAATA 300
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 Db 301 AAAAAATCTTTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTAAAAAAAT 360
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 Db 421 AGTTTGTCATTCGTTATATCGAGTCAATTAAGACATGCTCTACTCATCTCAATTTT 480
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 Db 541 AAGGTATTTAGGACACACTTTGTGCTCATGTGCATGTGTGATGACCTCTCATACAC 600
 Qy 601 GTTCAACTAGGACACATCTCCAAATATGCTCGCCATTTAAATATACATTAAGTAGAATA 660
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 Db 661 TCTGAATTCAGACACTTCAACATCAACAGACCACTTTTAATATATCTAAATACAAAA 720
 Qy 721 ATTAATTTTACAGATATGATGAAAGATAGAAACGAATATTTAGTTTTCACATACAA 780
 Db 721 ATTAATTTTACAGATATGATGAAAGATAGAAACGAATATTTAGTTTTCACATACAA 780
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 Db 781 AAAAAAAGATTTTGGTGTGCGGCGGAGCCAACTCCCAATTTGGGACACAGGCA 840
 Qy 841 CAACAGAGTGTGCGGCGGACAGAACCAACCAAAAAACGATATCTAACGAGACAGCA 900
 Db 841 CAACAGAGTGTGCGGCGGACAGAACCAACCAAAAAACGATATCTAACGAGACAGCA 900
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 Db 901 AGTCCGCAACACTTTTAAAGAGGCTTTGGCGGACAGAGAGAGAGAGAGAGAGAG 960
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 Qy 1141 TCCACTCTCTCTCAAGGATATGCGCTTGGTCTTGGATTTATGTTCTAGGT 1200
 Db 1141 TCCACTCTCTCTCAAGGATATGCGCTTGGTCTTGGATTTATGTTCTAGGT 1200
 Qy 1201 TGTGTAGTACGGGCGTTGATGTTAGAGAAAGGGATCTGATCTGTGATGATCTGTTCT 1260
 Db 1201 TGTGTAGTACGGGCGTTGATGTTAGAGAAAGGGATCTGATCTGTGATGATCTGTTCT 1260
 Qy 1261 TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGATCGGTTGCTGATTAAGT 1320

Db 1261 TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGGTTGGTTGATTAAGT 1320
 Qy 1321 ATGGTTTTCAATTCGCTGAGAGGCTCTATGAGAAATGAATAGTTTAAAGGTAACGAATCTT 1380
 Db 1321 ATGGTTTTCAATTCGCTGAGAGGCTCTATGAGAAATGAATAGTTTAAAGGTAACGAATCTT 1380
 Qy 1381 GCGATTTTGTGAGTACCTTTTGTGAGTAAATCAGAGACCGGTGATTTTGTGCTTGT 1440
 Db 1381 GCGATTTTGTGAGTACCTTTTGTGAGTAAATCAGAGACCGGTGATTTTGTGCTTGT 1440
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 Db 1501 AGCTATCCCTTGTATATCCCTATTTGAACAAAAATATCAACTTTGAAGAAGTCCCGT 1560
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 Db 1561 TGATGAGATTAATGATGATTTGATTTAGCTTCAAAATTTTCCGACGCTGCTTTAG 1620
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 Db 1621 ATACAGTATCCCATCAAGAAATTCATGAAACAGTATATATCTCAGAAACAGGGAT 1680
 Qy 1681 TCCCTGTCTTCCGATTTGCTTATAGTCCAGAAATTTTTCGCAATATCTTAAAAAGT 1740
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 Db 1741 CACTTTCGTTCACTTAATGAATGATTTGCTACAAATATATGCTTTATAGCTTATCC 1800
 Qy 1801 TAGCTGATGTTCACTTATAGTAATACCCCTATAGTTTATGTCAGAGAAACCTTATCC 1860
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 Qy 1861 GATTTCTGATCTCCATTTTATATATATGAAATGAACGTATGATGACAGAGAAACCTTATCC 1920
 Db 1861 GATTTCTGATCTCCATTTTATATATATGAAATGAACGTATGATGACAGAGAAACCTTATCC 1920
 Qy 1921 GGAATATTTTATTTATAGCTTTTCAACCCCTCATTTATCTGAGCTGAAAGTCTGCATGA 1980
 Db 1921 GGAATATTTTATTTATAGCTTTTCAACCCCTCATTTATCTGAGCTGAAAGTCTGCATGA 1980
 Qy 1981 ACTGTCCTCAATTTTGTGTTTCAAAATTCATGATGATATCTATGATATCTCTTGTATC 2040
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 Qy 2041 TACCTGTAGAAATTTTGTGTTATCTTGAACGCTGCTGATTAACAGAAAGAAATTTAT 2100
 Db 2041 TACCTGTAGAAATTTTGTGTTATCTTGAACGCTGCTGATTAACAGAAAGAAATTTAT 2100
 Qy 2101 GAACTGTATTCGGGATATGTTATCTGCTTCTTCTTATGATTAATCTTCTTGTGACATT 2160
 Db 2101 GAACTGTATTCGGGATATGTTATCTGCTTCTTCTTATGATTAATCTTCTTGTGACATT 2160
 Qy 2161 CTGCTGTAGCTGCACTTCAACAGCAAGTTCC 2195
 Db 2161 CTGCTGTAGCTGCACTTCAACAGCAAGTTCC 2195

RESULT 2
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 LOCUS O.sativa (rice) constitutive GOS2 gene.
 DEFINITION X51910
 ACCESSION X51910.1 GI:20237
 VERSION GOS2 gene; rice.
 KEYWORDS Oryza sativa (indica cultivar-group)
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

FEATURES	Location/Qualifiers
source	1. .3192

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polyA_signal	/number=5	3028
ORIGIN	/gene="G0S2"	
Query Match	97.6%	Score 2141.4; DB 15; Length 3192;
Best Local Similarity	99.1%;	Pred. No. 0;
Matches 2175; Conservativity	0;	Mismatches 16; Indels 4; Gaps 2
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Db	6 AATCGAAGAGTTCTCGACCGTTTTGACGTCCTCAACCAATATGAGGAACTGTGTCT	65
OY	61 AAATATATAATGAGACTTATATATGTAGCGCTGATTAATACTAGAACTATGTAAAGAAACT	120
Db	66 AAATATATAATGAGACTTATATATGTAGCGCTGATTAATACTAGAACTATGTAAAGAAACT	125
OY	121 CATCCACTTACTTATAGTGGCAATGGGCTAAATATATAAGAGTGGCTTCACTAGTTTGGT	180
Db	126 CATCCACTTACTTATAGTGGCAATGGGCTAAATATATAAGAGTGGCTTCACTAGTTTGGT	185
OY	181 TTCTCTTATATATTAAGTGGGAAAAATGAATCATATATGCTTAGAATATPAGTTCACATC	240
Db	186 TTCTCTTATATATTAAGTGGGAAAAATGAATCATATATGCTTAGAATATPAGTTCACATC	245
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Db	246 TCTGTCAATGAAGTAAATATATTCGAGTAGCCATATATGTCAATCAACTCTTCTTGAATA	305
OY	301 AAAAAATCTTCTAGCTGAACTCAATGGGTAAGAGAGATATTTTTTTTAAAAAAAAT	360
Db	306 AAAAAATCTTCTAGCTGAACTCAATGGGTAAGAGAGATATTTTTTTTAAAAAAAAT	362
OY	361 AGAATGAAGATATCTGAACGTATCCGAAAGATTATAACATATATATATATTTAT	420
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Db	663 ATCTGAATTCAGGACTTCAACCATACCGAGACCACTTTTAATATATATCTAAATATCAAAA	722
OY	720 AATATATTTACGAATATGACATGAAGAAAGTATGAACGAATCTATTAGTGTTCACATACA	779
Db	723 AATATATTTACGAATATGACATGAAGAAAGTATGAACGAATCTATTAGTGTTCACATACA	782
OY	780 AAAAAAATAAATTTTGTGCTGTCGAGGAGGCAATCTCCCATATTTGGGACACAGGACA	839
Db	783 AAAAAAATAAATTTTGTGCTGTCGAGGAGGCAATCTCCCATATTTGGGACACAGGACA	842
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Db	843 ACAACAGAGTGGCTGCCACAGAACCAACCAAAAAAGATGATCTTAACGAGGACAGC	902
OY	900 AAGTCCGCAACACTTTTAAACAGAGGCTTTGGGCCAGAGAGAGAGAGAGGCAAA	959

Db	903	AAGTCCGCAACAACTTTTAAACAGAGGCTTTGCGCCAGAGAGAGGAGAGGCAAA	962
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Db	963	GAAAAACAAGACATCTCTCTCCCTCCCATATATAATTCCTCCCCCTTTTCCCTCTCAT	1022
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Qy	1140	CTCCACCTTCCTCTCAACAGGGATAGTGCCTTCGGTGTCTTGGATTATTTGTTCAAG	1199
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Qy	1380	TGCGATTTTGAGAGTACCTTTGTTTGAGGTAAATCGAGACACGGGATTTTGCTTGG	1439
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Qy	1440	TGTAATTAAGTACATTTGTTTGGTCTCGATTCGTAGTAGTGTCTCGATTTGACG	1499
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Qy	1500	AAGTATCTCTTGTATTTCCTCATTTGAACAAAATAATCCAACCTTGAGAGCGTCCG	1559
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Db	1563	TTGATGAAATTTGAATGATTTCTTAAGCCGTGCCAAATTTGCGAGCTGGCTGTGTTA	1622
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Db	1623	GATACAGTAGTCCCATCATCAGAAATTCATGAAACAGTTATATCTTCAGGAAACAGGGGA	1682
Qy	1680	TTCCCTGTCTTCGCAATTTGCTTAGTCCAGAAATTTTTTCCCAATATCTTAAAAAG	1739
Db	1683	TTCCCTGTCTTCGCAATTTGCTTAGTCCAGAAATTTTTTCCCAATATCTTAAAAAG	1742
Qy	1740	TCACTTTCGGTTCAGTTCATGAAATGATGTGTCATAAATAAGCTTTTATAGGTTATC	1799
Db	1743	TCACTTTCGGTTCAGTTCATGAAATGATGTGTCATAAATAAGCTTTTATAGGTTATC	1802
Qy	1800	CTAGCTGATGTCAGTTATATAGTAAACCCCTATAGTTTAGTCAGAGAGAACTTATC	1859
Db	1803	CTAGCTGATGTCAGTTATATAGTAAACCCCTATAGTTTAGTCAGAGAGAACTTATC	1862
Qy	1860	CGATTTTCGATCTCCATTTTATATATATGAAATGAACGTAGACATAAGCAGTATTCAT	1919
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Qy	1920	TGATATATTTTATTTATTAAGCTTTCAACCCCTTCATATCTTGAGCTGAAAGTCTGGCAT	1979
Db	1923	TGATATATTTTATTTATTAAGCTTTCAACCCCTTCATATCTTGAGCTGAAAGTCTGGCAT	1982
Qy	1980	AACGTCTCTCAATTTTGTATTTCAAAATTCACATGATATCTATGATATCTCTGTAT	2039
Db	1983	AACGTCTCTCAATTTTGTATTTCAAAATTCACATGATATCTATGATATCTCTGTAT	2042

QY	2040	CTACCTGTAGAAGTTCTTTTGGTATTCCTTACCTGCTGATTACGAAAGAAATTTA	2099
DB	2043	CTACTGTGAGAAGTTCTTTTGGTATTCCTTACCTGCTGATTACGAAAGAAATTTA	2102
QY	2100	TGAAGCTGTAAATCGGATATGTTATATATGCTGTTGTTCTTATGATTCATTTCTTTGTGCACT	2155
DB	2103	TGAAGCTGTAAATCGGATATGTTATATGCTGTTGTTCTTATGATTCATTTCTTTGTGCACT	2162
QY	2160	TCTTGGTGTAGCTTGCCACTTTCACACGAAAGTT	2194
DB	2163	TCTTGGTGTAGCTTGCCACTTTCACACGAAAGTT	2197
RESULT 3			
LOCUS	C0895917	3032 bp	DNA linear PAT 05-NOV-2004
DEFINITION	Sequence 7 from Patent WO2004090142.		
ACCESSION	C0895917		
VERSION	C0895917.1	GI:55467905	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE	1		
AUTHORS	Sanz Molinero, A.I.		
TITLE	Plants having modified growth characteristics and method for making the same		
JOURNAL	Patent: WO 2004090142-A 7 21-OCT-2004;		
FEATURES	CropDesign N.V. (BE)		
source	Location/Qualifiers		
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	/note="expression cassette for MT2a"		
ORIGIN			
Query Match	97.5%; Score 2139.2; DB 6; Length 3032;		
Best Local Similarity	99.0%; Pred. No. 0;		
Matches 2174; Conservative	0; Mismatches 18; Indels 4; Gaps 2;		
QY	1	AATCGGAAAAGTTCTGACCGCTTTTACCGCTTACCTAACATATATAGGAACGTGCT	60
DB	1	AATCGGAAAAGTTCTGACCGCTTTTACCGCTTACCTAACATATATAGGAACGTGCT	60
QY	61	AAATATAAATGAGACCTTATATATATGAGCGCTGATTACTGAACTATGTAAAGAAAAC	120
DB	61	AAATATAAATGAGACCTTATATATATGAGCGCTGATTACTGAACTATGTAAAGAAAAC	120
QY	121	CATCACCTACTTATAGTGGCAATCGGGCTAAATAAAAAGATGGCTACACTAGTTTGT	180
DB	121	CATCACCTACTTATAGTGGCAATCGGGCTAAATAAAAAGATGGCTACACTAGTTTGT	180
QY	181	TTTCCCTTAGTAAATTAAGTGGGAAAAATGAAATCATTAATGCTTAAGATTAAGTCAACATC	240
DB	181	TTTCCCTTAGTAAATTAAGTGGGAAAAATGAAATCATTAATGCTTAAGATTAAGTCAACATC	240
QY	241	TCTGTCAATGAAGTAAATTAATTCGAGGTAGCATTAATGTCATCAAACTCTTCTTGATA	300
DB	241	TCTGTCAATGAAGTAAATTAATTCGAGGTAGCATTAATGTCATCAAACTCTTCTTGATA	300
QY	301	AAAAAATCTTCTTAGCTGAACCTCAATGGGTAAAGAGAGATTTTTTTTTTAAAAAAAAT	360
DB	301	AAAAAATCTTCTTAGCTGAACCTCAATGGGTAAAGAGAGATTTTTTTTTTAAAAAAAAT	360
QY	361	AGAAATGAAGATTTCTGAACGTATCGGCAAAAGATTTTAACTATATATATATATTTAT	420
DB	361	AGAAATGAAGATTTCTGAACGTATCGGCAAAAGATTTTAACTATATATATATATTTAT	420
QY	421	AGTTTGATCATGTTTATATGACGTCATTAAGACATGCTTAACTCACTCAATTTT	480
DB	421	AGTTTGATCATGTTTATATGACGTCATTAAGACATGCTTAACTCACTCAATTTT	480
QY	477	AGTTTGATCATGTTTATATGACGTCATTAAGACATGCTTAACTCACTCAATTTT	537
DB	477	AGTTTGATCATGTTTATATGACGTCATTAAGACATGCTTAACTCACTCAATTTT	537

QY	481	TATTTAGTAATTAAAGACAATTGACTATTTTTTATTTATTTATCTTTTTTCGATTAATGC	540
DB	478	TATTTAGTAATTAAAGACAATTGACTATTTTTTATTTATTTATCTTTTTTCGATTAATGC	537
QY	541	AAGGTACTTAAGCACAACCTTTGTGTCTAATGTGATGTGAGTGCACCTCCCTC-ATACA	599
DB	538	AAGGTACTTAAGCACAACCTTTGTGTCTAATGTGATGTGAGTGCACCTCCCTCAATAC	597
QY	600	CGTTCACTAGCGACACATCTCCCAATATGACTCGCCTATTTTATATCACTTTAGGTAGCAAT	659
DB	598	CGTTCACTAGCGACACATCTCTAATATCACTCGCCTATTTTATATCACTTTAGGTAGCAAT	657
QY	660	ATCTGAATTCAGACACTTACCATCACTACAGACACACTTTTAAATATCTTAAATACAAA	719
DB	658	ATCTGAATTCAGACACTTACCATCACTACAGACACACTTTTAAATATCTTAAATACAAA	717
QY	720	AATATATTTTACGAATAGCATGAAAGTAAGTAAGAACATATTTAGTCTTTTACATAC	779
DB	718	AATATATTTTACGAATAGCATGAAAGTAAGTAAGAACATATTTAGTCTTTTACATAC	777
QY	780	AAAAAAAAAAGATTTTGTCTGTGCGCGAGCCCAATCTCCCATATTTGGGCAACAAGCA	839
DB	778	AAAAAAAAAAGATTTTGTCTGTGCGCGAGCCCAATCTCCCATATTTGGGCAACAAGCA	837
QY	840	ACAACAGAGTGGCTGGCCACAGAACAAACCACAAAAACGATGATCTAAACGAGACAC	899
DB	838	ACAACAGAGTGGCTGGCCACAGAACAAACCACAAAAACGATGATCTAAACGAGACAC	897
QY	900	AAGTCCGCAACAACCTTTTAAACAGACAGGCTTTTGGGCCCAGAGAGAGAGAGAGGCAAA	959
DB	898	AAGTCCGCAACAACCTTTTAAACAGACAGGCTTTTGGGCCCAGAGAGAGAGAGAGGCAAA	957
QY	960	GAATAACAGCAATCCCTCCTCCCTCCCATCTATATAATCTCCGCCCTTTTCCCTCTAT	1011
DB	958	GAATAACAGCAATCCCTCCTCCCTCCCATCTATATAATCTCCGCCCTTTTCCCTCTAT	1011
QY	1020	ATAGAGGCGATCCAAAGCCAAAGAGAGGAGAGACCAAGAGACACGCGACTAGCAGAAGCC	1077
DB	1018	ATAGAGGCGATCCAAAGCCAAAGAGAGGAGAGACCAAGAGACACGCGACTAGCAGAAGCC	1077
QY	1080	GAGGACCGGCTTTCTTCGATCCATATCTTCCGGTGAATTTCTTGGTGCATCTCTCCCTC	1133
DB	1078	GAGGACCGGCTTTCTTCGATCCATATCTTCCGGTGAATTTCTTGGTGCATCTCTCCCTC	1133
QY	1140	CTCCACCTCCTCTCAACAGGGATATGAGCCCTTCGGTGTCTTGAATTTATGTTCTAG	1199
DB	1138	CTCCACCTCCTCTCAACAGGGATATGAGCCCTTCGGTGTCTTGAATTTATGTTCTAG	1199
QY	1200	TTGTGTAGTACGGGCGTTGATGTTAAGAAAGGGGATCTGTATCTGTAGATTTCCGTTC	1255
DB	1198	TTGTGTAGTACGGGCGTTGATGTTAAGAAAGGGGATCTGTATCTGTAGATTTCCGTTC	1255
QY	1260	TTGATTTGGATATAGAGGGGTTCTTGATTTGTCAATGTTATCGGTTCCGTTTGAATAGT	1311
DB	1258	TTGATTTGGATATAGAGGGGTTCTTGATTTGTCAATGTTATCGGTTCCGTTTGAATAGT	1311
QY	1320	TATGTTTTCATTCGTCTTGAGAGCTATATGAAATGAATGGTTTAAAGGTACGGAATCT	1377
DB	1318	TATGTTTTCATTCGTCTTGAGAGCTATATGAAATGAATGGTTTAAAGGTACGGAATCT	1377
QY	1380	TGCGATTTTGTAGTACCTTTTGTTTGAGTAAATCAGAGCACCGGTATTTTGGCTTG	1433
DB	1378	TGCGATTTTGTAGTACCTTTTGTTTGAGTAAATCAGAGCACCGGTATTTTGGCTTG	1433
QY	1440	TGTATTAATAAGTACATTTGTGTGCTCTCGATTTCTGTAGTATGCTTCTGCATTTGAAG	1499
DB	1438	TGTATTAATAAGTACATTTGTGTGCTCTCGATTTCTGTAGTATGCTTCTGCATTTGAAG	1499
QY	1500	AAGCTATCTTTGTTTATTTCCCTATTTGAACAAAATATATCCAACTTTGAAGACGGTCCG	1555
DB	1498	AAGCTATCTTTGTTTATTTCCCTATTTGAACAAAATATATCCAACTTTGAAGACGGTCCG	1555

Oy		1560	TTGATAGATATGAATGATATGGATTCTTAAACCGTCGCCAAAATTTGGCAGCTGGCTGTGTTA	1619			
Db		1558	TTGATGAATTAAGAATGATGATTCCTTAAGCCCTGCACAAAATTTGGCAGCTGGCTGTGTTA	1617			
Oy		1620	GATACAGTAGTCCCCCATCAACAATAATCATGAAAAAGTTATATATCTTCAGGAACAGGGGA	1679			
Db		1618	GATACAGTAGTCCCCCATCAACAATAATCATGAAAAAGTTATATATCTTCAGGAACAGGGGA	1677			
Oy		1680	TTCCCTGTTCTCCGAAATTCCTTTAGTCCCGAAATTTTTTCCCAGAAATATCTTAAAAAG	1739			
Db		1678	TTCCCTGTTCTCCGAAATTCCTTTAGTCCCGAAATTTTTTCCCAGAAATATCTTAAAAAG	1737			
Oy		1740	TCACTTTTCGGTTCAGTTCGAATGAATGATTGCTACAAATATACCTTTTATAGGCTATC	1799			
Db		1738	TCACCTTCCTGGTTCAGTTCGAATGAATGATTGCTACAAATATATGCTTTTATAGGCTATC	1797			
Oy		1800	CTAGCTGAGTTCAGTTATATAGTAATACCCTTATAGTTAGTCAGGAGAAACTATATC	1859			
Db		1798	CTAGCTGAGTTCAGTTATATAGTAATACCCTTATAGTTAGTCAGGAGAAACTATATC	1857			
Oy		1860	CGATTTCTGATCTCCATTTTTTAATTAATATGAATAAGAACTGTAGCATTAAGCATATTCATT	1919			
Db		1858	CGATTTCTGATCTCCATTTTTTAATTAATATGAATAAGAACTGTAGCATTAAGCATATTCATT	1917			
Oy		1920	TGATATATTTTTTTTATTAAGCTTTCACCCCTCTCATATTTCTGAGCTGAAAGTCTGGCATG	1979			
Db		1918	TGATATATTTTTTTTATTAAGCTTTCACCCCTCTCATATTTCTGAGCTGAAAGTCTGGCATG	1977			
Oy		1980	AACGTGCTCAATTTTGTTTCAAAATTCACATCGATATATCATGATATATCCTTGAT	2039			
Db		1978	AACGTGCTCAATTTTGTTTCAAAATTCACATCGATATATCATGATATATCCTTGAT	2037			
Oy		2040	CTACCTGAGAAAGTTCCTTTTGGTATATTCCTTGACTGCTGATTACAGAAAGAAATTTA	2099			
Db		2038	CTACCTGAGAAAGTTCCTTTTGGTATATTCCTTGACTGCTGATTACAGAAAGAAATTTA	2097			
Oy		2100	TGAAGCTGTAATCGGAGATAGTTATATACGTCTGTTCTTATGATTCATTTCCTTGTGCACT	2159			
Db		2098	TGAAGCTGTAATCGGAGATAGTTATATACGTCTGTTCTTATGATTCATTTCCTTGTGCACT	2157			
Oy		2160	TCTTGCTGCTAGCTTGCCACTTTTACCCAGCAAAGTTC	2195			
Db		2158	TCTTGCTGCTAGCTTGCCACTTTTACCCAGCAAAGTTC	2193			
RESULT 4							
LOCUS	BD251965/c		9361 bp	DNA linear PAT 17-JUL-2003			
DEFINITION	Artificial matrix attachment region for increasing expression of genes introduced in plant cells.						
ACCESSION	BD251965						
KEYWORDS	BD251965.1 GI.33061735						
SOURCE	JP 2002531097-A/27.						
ORGANISM	synthetic construct						
REFERENCE	other sequences; artificial sequences.						
AUTHORS	1 (bases 1 to 9361)						
	Geest,A.H.V.D., Ainley,M.W., Cowen,N.M., Welter,M.E. and						
	Wooley,A.T.						
TITLE	Artificial matrix attachment region for increasing expression of genes introduced in plant cells						
JOURNAL	Patent: JP 2002531097-A 27 24-SEP-2002;						
COMMENT	DOW AGROSCIENCES LLC						
	OS Artificial Sequence						
	PN JP 2002531097-A/27						
	PD 24-SEP-2002						
	PF 30-NOV-1999 JP 2000585431						
	PR 01-DEC-1998 US 60/110437						
	PI APOLONTIA HM VAN DER GEEST,MICHAEL W AINLEY,NEIL M COWEN,MARY E						
	PI WELTER,						
	PI AARON T WOOLEY						
	PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC						

Description of Artificial Sequence:pgos2-hpt
FH Key Location/Qualifiers
FT source 1..9361
FT /organism='Artificial Sequence'.
location/Qualifiers

1..9361
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 97.2%; Score 2133.4; DB 6; Length 9361;

Beet Local Similarity 99.1%; Pred. No. 0;

Matches 2167; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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DB 7083 AGTTCTGACCGCTTTTCAGCTGCTTACCTAACATATAGAGAAAGTGTCTAAATATAA 7024
QY 70 ATGAGACCTTATATATATAGCGCTGATTACTAGAACTATGTAAAGAAAACTCATCCACT 129
DB 7023 ATGAGACCTTATATATATAGCGCTGATTACTAGAACTATGTAAAGAAAACTCATCCACT 6964
QY 130 ACTTATAGTGGCAATGGGCTAAATATAAAGAGTGGCTACACTAGTTGCTTTCTTCTAG 189
DB 6963 ACTTATAGTGGCAATGGGCTAAATATAAAGAGTGGCTACACTAGTTGCTTTCTTCTAG 6904
QY 190 TAAATTAAGTGGAAATGAAATCATTTATGCTTAAGATATAGCTTACACTCTGTGATG 249
DB 6903 TAAATTAAGTGGAAATGAAATCATTTATGCTTAAGATATAGCTTACACTCTGTGATG 6844
QY 250 AAGTTAAATTAATTCAGAGTACCATAATTTGTCATCAAACTCTCTTGAATAAAAAATCT 309
DB 6843 AAGTTAAATTAATTCAGAGTACCATAATTTGTCATCAAACTCTCTTGAATAAAAAATCT 6784
QY 310 TTCTAGCTGAATCTCAATGGGTAAAGAGATAATTTTTTAAAAAAAATGAATGAG 369
DB 6783 TTCTAGCTGAATCTCAATGGGTAAAGAGATAATTTTTTAAAAAAAATGAATGAG 6727
QY 370 ATATTCTGAACGTATCGGCAAGATTAAACATATATATATATATATATATATATATATGTC 429
DB 6726 ATATTCTGAACGTATCGGCAAGATTAAACATATATATATATATATATATATATATATGTC 6667
QY 430 ATTCTTATATCGACGTTCATTAGAGACATGTCTTACTCCATCTCAATTTTTTATTTAGTA 489
DB 6666 ATTCTTATATCGACATCATTTAAGACATGTCTTACTCCATCTCAATTTTTTATTTAGTA 6607
QY 490 ATTTAAAGACAATTGACTTATTTTTTATTTATTTATCTTTTTTGCATTNAGATGCAAGTACTT 549
DB 6606 ATTTAAAGACAATTGACTTATTTTTTATTTATTTATCTTTTTTGCATTNAGATGCAAGTACTT 6547
QY 550 AGGCACACACTTGTGCTGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 608
DB 6546 AGGCACACACTTGTGCTGATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTC 6487
QY 609 AGCGACACATCTCAATATCACTCGCTATTTTATATACATTTAGTGAACAATCTGAATT 668
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DB 6366 ACAGAAATGATGAAGAAAGTATGAAGAACTATTTAGTTTTTTCATACAAAAAATAA 6307
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QY 969 GCATCTCTCTCTCTCCCATCTATTAATTCCTCCCTTTTCCCTCTCTATATAGAGGC 1028
DB 6126 GCATCTCTCTCTCTCCCATCTATTAATTCCTCCCTTTTCCCTCTCTATATAGAGGC 6067
QY 1029 ATCCAGGCAAGAGAGGAGAGACCAAGACACAGCACTAGACAGAAAGCCAGACCG 1088
DB 6066 ATCCAGGCAAGAGAGGAGAGACCAAGACACAGCACTAGACAGAAAGCCAGACCG 6007
QY 1089 CTTCTCTGATCCATATCTTCGCGTCCAGTCTTGTGATCTCTTCTCTCCACTC 1148
DB 6006 CTTCTCTGATCCATATCTTCGCGTCCAGTCTTGTGATCTCTTCTCTCCACTC 5947
QY 1149 CTCTCACAAGGATATGTCCTTGTGCTTCTGATTTATTTGTTCTAGAGTTGTAGT 1208
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QY 1269 GGATAGAGGGTCTTGAATGTTGATGTTATCGGTTCTGTTGATAGTATGATGTTT 1338
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DB 5766 CAATGCTTGAAGAGCTTATAGAAATGAATGTTATAGGTACGGAATCTTGGATT 5707
QY 1389 GTGAGTACCTTTTGTGAGGTAATACAGACACCGGTATTTGCTTGGTATATAA 1448
DB 5706 GTGAGTACCTTTTGTGAGGTAATACAGACACCGGTATTTGCTTGGTATATAA 5647
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DB 5646 AGTACGTTGTTGTGCTCGATTTCTGATGATGCTTCTGATTTGACGAACATGCT 5587
QY 1509 TTTGTTTATTCCTTATTTGAACAAATATATCAACTTTGAAGAGGTCCTGTATAGA 1568
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QY 1569 TTGAATGATGATTTCTTAAGCTGTCGCAAAATTTGAGCTGGCTGTTGATATACGTA 1628
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QY 1629 GTCCCATCAAGAAATTCATGAAAAAGTTTAAATCTTCAGGAAACAGGGATTCCTGTT 1688
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QY 1749 GGTTCAGTTCAATGAATGATTTGTCACAAATATATGCTTTTATAGCTTATCTAGCTGTA 1808
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QY 1869 ATCTCATTTTAAATATATATGAATGAATCTATAGCATAGAGATTTCACTTTGATTTT 1928
DB 5226 ATCTCATTTTAAATATATGAATGAATCTATAGCATAGAGATTTCACTTTGATTTT 5167
QY 1929 TTTTATTTTACCTTCCCTTCAATTTCTGATTTCTGAGCTGAAGTCTGGGATGAACGTGCT 1988
DB 5166 TTTTATTTTACCTTCCCTTCAATTTCTGAGCTGAAGTCTGGGATGAACGTGCTGCT 5107
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Qy		1989	CAATTTGTTTTCAAATTACAGATGCATTAATCAGATTCCTGTGATCTACCTGA	2048
Dd		5106	CAATTTTGTTTTCAAATTCACATCGATTAATCATATGATTAATCCCTGTATCTACCTGA	5047
Qy		2049	GAA GTTTC TTTTGGTATATCTTACACGCTGATTAACAAGAAAAGAAATTTATGAAGCTGT	2108
Dd		5046	GAA GTTTC TTTTGGTATATCTTACACGCTGATTAACAAGAAAAGAAATTTATGAAGCTGT	4987
Qy		2109	AATCGGATAGTAAATAGCTGTTGTTCTTAATGAATTCATTTCTTTGTCAGTTCTTGCTGT	2168
Dd		4986	AATCGGATAGTAAATAGCTGTTGTTCTTAATGAATTCATTTCTTTGTCAGTTCTTGCTGT	4927
Qy		2169	AGCTTGCCA CTTCACGCAAGAAGTTC	2195
Dd		4926	AGCTTGCCA CTTCACGCAAGAAGTTC	4900
RESULT 5				
BDS21966/c				
LOCUS		BDS21966	10629 bp	DNA linear PAT 17-JUL-2003
DEFINITION		Artificial matrix attachment region for increasing expression of genes introduced in plant cells.		
ACCESSION		BDS21966		
VERSION		BDS21966.1	GI:33061736	
KEYWORDS		JP 2002531097-A/28.		
SOURCE		JP 2002531097-A/28.		
ORGANISM		synthetic construct other sequences: artificial sequences. 1 (bases 1 to 10629) Geelc,A.H.V.D., Ainley,M.W., Cowen,N.M., Welter,M.E. and Woosley,A.T.		
REFERENCE		Artificial matrix attachment region for increasing expression of genes introduced in plant cells Patent: JP 2002531097-A 28 24-SBP-2002;		
AUTHORS		DOW AGROSCIENCES LLC		
TITLE		OS Artificial Sequence		
JOURNAL		PN JP 2002531097-A/28		
COMMENT		PD 24-SBP-2002 PF 30-NOV-1999 JP 2000585431 PR 01-DEC-1998 US 60/110437 PI APOLO니아 HM VAN DER GEBST,MICHAEL W AINLEY,NEIL M COWEN,MARY E		
FEATURES		PI WELTER, PI AARON T WOOSLEY PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC Description of Artificial Sequence:PARCOS2AF-hpc FH Key Location/Qualifiers FT source 1..10629 /organism='Artificial Sequence'. location/Qualifiers 1..10629 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"		
ORIGIN				
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Best Local Similarity		99.1%;	Pred. No. 0;	
Matches 2167;		Conservative 0;	Mismatches 16;	Indels 4; Gaps 2;
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Qy		70	ATGAGACCTTATATATATGATGCGCTGATTAATGAACATATGTAAGAAAACTCATCACT	129
Dd		7662	ATGAGACCTTATATATATGATGCGCTGATTAATGAACATATGCAAGAAAACTCATCACT	7603
Qy		130	ACTTAGTAGGCAATGCGGCTAAATATAAAAGATGCTACACTAGTTTCGTTTTCTTAG	189
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QY	190	TAATTAATCGGAAAATGCAATTCATTTATGCTTGAATAATACGTTCAATCTGTCAG	249
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QY	250	AAGTTAAATTTATGAGGATGACCCATTAATTGTCATCAAACTCTCTTGAATAAAAAACT	309
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QY	310	TTTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTTAAAAAAAATGAAATGAAG	369
Db	7422	TTTAGCTGAACTCAATGGGTAAAGAGAGATATTTTTTTTTAAAAAAAATGAAATGAAG	7366
QY	370	ATATTCTGAACGTATCGGCAGAAAGTTTAAACATATATATATATATATATATAGTTGCG	429
Db	7365	ATATTCTGAACGTATGCGCAAGATTTTAAACATATATATATATATATATATAGTTTGGC	7306
QY	430	ATTGCTTATTCGACCGTCATTTAAGAGACATGTCCTTACCTCAATTTTTTATTTAGTA	489
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QY	609	AGCAGCATCTCCAAATATCTCGGCCATTTATTAATACATTTAAGGAGCAATCTGAATT	668
Db	7125	AGCAGCATCTCTTAATATCTCGGCCATTTATTAATACATTTAAGGAGCAATCTGAATT	7066
QY	669	CAAGCACTTCACCATCACAGACCACTTTTAAATATCTAAAAATACAAAAATTAATTT	728
Db	7065	CAAGCACTTCACCATCACAGACCACTTTTAAATATCTAAAAATACAAAAATTAATTT	7006
QY	729	ACAGAAATGCAATGAAAAAGTATGAAACGACATTTTAGTTTTTCAATACAAAAAAA	788
Db	7005	ACAGAAATGCAATGAAAAAGTATGAAACGACATTTTAGTTTTTCAATACAAAAAAA	6948
QY	789	AGAAATTTGCTCGTGCGGAGCGGCATCTCCCATTTGGGCACACAGGCAACAACAG	848
Db	6945	AGAAATTTGCTCGTGCGGAGCGGCATCTCCCATTTGGGCACACAGGCAACAACAG	6886
QY	849	TGGCTGCCACAGAACCAACCAAAAAACGATGATCTAACGAGGAGCAGCAAGTCCCA	908
Db	6885	TGGCTGCCACAGAACCAACCAAAAAACGATGATCTAACGAGGAGCAGCAAGTCCCA	6822
QY	909	ACAACCTTTTAAACAGACGCTTTTCGCGCAGAGAGAGAGAGAGCAAGCAAGAAACCA	968
Db	6825	ACAACCTTTTAAACAGACGCTTTTCGCGCAGAGAGAGAGAGAGCAAGCAAGAAACCA	6766
QY	969	GCATCTCTCTCTCCCATCTATAATTTCTTCCCCCTTTTCCCTCTCTATATAGGAAGC	1022
Db	6765	GCATCTCTCTCTCCCATCTATAATTTCTTCCCCCTTTTCCCTCTCTATATAGGAAGC	6706
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QY	1149	CTCTCTCAAGGATATGTCCTCTTGCTGTTGTTCTTGGAATTAATGTTCTAGGTTGTAAGT	1208
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QY	1209	ACGGAGCGTTATGTTAAGAAAGGGAGTCTGTATCTGTAGATATCTCTGTTCTTGGAATTTG	1268
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LOCUS Oryza sativa (japonica cultivar-group) chromosome 7 clone
DEFINITION OJ1365_D04, *** SEQUENCING IN PROGRESS ***
ACCESSION AP003953
VERSION AP003953.1 GI:15021923
KEYWORDS HTG; HTS; PHASE2.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone: OJ1365_D04
JOURNAL Published Only in Database (2001)
REFERENCE
AUTHORS 2 (bases 1 to 105692)
TITLE Sasaki, T., Matsumoto, T. and Yamamoto, K.
JOURNAL Direct Submission
Submitted (25-JUN-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Matches 2183; Conservative 0; Mismatches 9; Indels 6; Gaps 4;
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81212 ACGAAGCTATCTTTGTTTATCCCTATTTGAAACAAATATCAACTTTGAAAGCGGTC 81153
1557 CCGTTGATGAGATGATGATTTGATTTTAAAGCTGTCCAAATTTCCAGCTGCTGT 1616
81152 CCGTTGATGAGATGATGATTTGATTTTAAAGCTGTCCAAATTTCCAGCTGCTGT 81093
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CDS
pseudogene, transposase"
pseudo
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D41499(S4032), AU094265(E3758), AU033141(S4032)
contains full-length cDNA(s) : AK099918"
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AALFTSTWSRLARPNVYKLFNAVAEDLIVKSGRGGVVTNALVSMNHDPQSCMDP
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probably inactive due to including stop codon(s) in CDS"
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Best Local Similarity 99.3%; Pred. No. 0;
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1 AATCCGAAAGTTTTCACCGTTTTCAGCTCTTAACAATATAGGAACTGTGCT 60
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61 AATATTAATGACCTTATATATATAGCGCTGATTAAGTATATGTAAGAAAACT 120
Db AATATTAATGACCTTATATATATAGCGCTGATTAAGTATATGTAAGAAAACT 35341
121 CATCCACCTACTTGTGCGCAATCGGGCTAAATTAAGGAGCGTACACTAGTTTCT 180
Db CATCCACCTACTTGTGCGCAATCGGGCTAAATTAAGGAGCGTACACTAGTTTCT 35340
181 TTTCTTAAATTAAGTGGGAAATGAATCATTAATTCCTTAAGATATAGCTTCATC 240
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241 TTTCTTAAATTAAGTGGGAAATGAATCATTAATTCCTTAAATATAGCTTCATC 35221
35280 TTTCTTAAATTAAGTGGGAAATGAATCATTAATTCCTTAAATATAGCTTCATC 35221
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301 AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATTTTTTTTAAAAAAAT 360
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361 AGATGAAGATATTCGAACGATCGGCAAAATTTAAACATATATATATATTTAT 420
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35100 AGATGAAGATATTCGAACGATCGGCAAAATTTAAACATATATATATTTAT 35041
421 AGTTGTGATTCGTTATATGACGCTATTAAGACATGTCTTACTCATCTCAATTT 480
Db AGTTGTGATTCGTTATATGACGCTATTAAGACATGTCTTACTCATCTCAATTT 35040
481 TATTATGTAATTAAGACATGACTTATTTTATATATCTTTTTCGATTGATGAC 540
Db TATTATGTAATTAAGACATGACTTATTTTATATATCTTTTTCGATTGATGAC 34980
541 AAGGTACTTACGACACATCTTGTGCTCATGTGATGATGACCTCTC-ATAGA 599
Db AAGGTACTTACGACACATCTTGTGCTCATGTGATGATGACCTCTC-ATAGA 34920
599 AAGGTACTTACGACACATCTTGTGCTCATGTGATGATGACCTCTC-ATAGA 34861
34920 AAGGTACTTACGACACATCTTGTGCTCATGTGATGATGACCTCTC-ATAGA 34861
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659 CGTTCACTAGGACACATCTCAATATGCTCGCTATTTAATACATTTAGGTACAT 34801
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 Db 34081 TCTTGGATTTTGTGAGTACCTTTTGTGAGGTTAAATCAGAGCACCGGATTTTGTCT 34022
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 Db 33962 ACGAAGCTATCTTGTGTTTATCCCATTTGAACAAAATATCCACTTTTGAAGCGGTC 33903
 QY 1557 CCGTGTATGATGATGATGATGATTTCTTAAGGCTGTCCAAAATTTCCGAGCTGCTGT 1616
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 QY 1857 ATCCGATTTTCGATCTCCATTTTATATATGAAATGAACGTGATGATGATGATGATGATG 1916
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 QY 1917 ATTTGGATTTATTTTATATATGATGATGATGATGATGATGATGATGATGATGATGATG 1976
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 Db 33302 AGTTCTTGTGTAGTTCGCACTTTCACACGCAAAAGTT 33265
 RESULT 9
 AF294979 14203 bp DNA circular SYN 24-MAY-2002
 LOCUS AF294979
 DEFINITION Binary vector pINDEXT1, complete sequence.
 ACCESSION AF294979
 VERSION AF294979.1 GI:11559663
 KEYWORDS
 SOURCE
 ORGANISM
 Binary vector pINDEXT1
 other sequences; artificial sequences; vectors.
 REFERENCE
 1 (bases 1 to 14203)
 Ouwkerk,P.B., de Kam,R.J., Hoge,J.H. and Meijer,A.H.
 Glucocorticoid-inducible gene expression in rice
 JOURNAL Planta 213 (3), 370-378 (2001)
 PUBMED 11506359
 REFERENCE
 2 (bases 1 to 14203)
 Ouwkerk,P.B.F.
 Direct Submission
 Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute
 for Molecular Plant Sciences, Wassenaarseweg 64, Leiden 2333 AL,
 Netherlands
 COMMENT
 pINDEXT1 is a binary vector designed for glucocorticoid-inducible
 gene expression in plants and is optimized for use in rice; pINDEXT1
 is part of a series of four pINDEXT vectors (Genbank Accession
 Numbers AF294979-AF294982). pINDEXT vectors are based on parts of
 pCAMBIA-1300 encoded by Genbank Accession Number AF234296 and
 pTA1002 (Aoyama, T. and Chua N.-H., 1997, Plant J. 11:605-612).
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 1195..2157
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 2158..3552
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promoter
4357..4427
/note="containing 4 upstream activation sites; tetramer of
the GVG binding site"
4474..4531
/note="CamV 35S"
4548..4583
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sites XhoI, SpeI and SmaI"
4587..5055
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5332..5357
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Matches 2176; Conservative 0; Mismatches 16; Indels 8; Gaps 3;
QY 1 AATCCGAAAAGTTTCGACCGGTTTTCAGTCTTAACAATATAGGAAAGTGTGCT 60
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Db 93 AATATTAATAGACCTTATATATAGCGCTGATTAACCTAGAACCTATTAAGAAAACCT 152
QY 121 CATTCACCTACTTATAGTGGCAATCGGGCTAAATTAATAAAGAGTCCGTACA---CTAGTT 176
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QY 297 AATTAATAAATCTTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTTTTTAAAAAA 356
Db 333 AATTAATAAATCTTTCTAGCTGAACCTCAATGGGTAAAGAGAGATTTTTTTT---AAAA 389
QY 357 AATTAATAAATGAATATTTCTGAACCTATCGGAAAGATTTAAACATATATATATATTT 416
Db 390 AATTAATAAATGAATATTTCTGAACCTATTTGGCAAGATTTTAAACATATATATATATTT 449
QY 417 TTATATGTTTGTGATCTGTTATATGACAGTCAATTAAGACATGCTTACTCATCTCA 476
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Db 690 CATATCTGAATTAAGACCTTACACATCAACGACCACTTTTAATTAATCTAAATATAC 749
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 DB 2190 CAGTCTTGCTGTAGCTTGCATTTACACAGAAAGTTC 2229

RESULT 10
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 ACCESSION AF294980
 VERSION AF294980.1 GI:11559666
 KEYWORDS
 SOURCE
 ORGANISM
 Bacteria
 Binary vector pINDEX2
 Bacteria
 other sequences; artificial sequences; vectors.
 REFERENCE
 1 (bases 1 to 14230)
 Ouwkerk, P.B., de Kam, R.J., Hoge, J.H. and Meijer, A.H.
 Glucocorticoid-inducible gene expression in rice
 Planta 213 (3), 370-378 (2001)
 PUBMED
 11506359
 2 (bases 1 to 14230)
 Ouwkerk, P.B.F.
 Direct Submission
 Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute
 for Molecular Plant Sciences, Wassenaarseweg 64, Leiden 2333 AL,
 Netherlands
 COMMENT
 pINDEX2 is a binary vector designed for glucocorticoid-inducible
 gene expression in plants and is optimized for use in rice; pINDEX2
 is part of a series of four pINDEX vectors (Genbank Accession
 Numbers AF294979-AF294982). pINDEX vectors are based on parts of
 pCAMBIA-1300 encoded by Genbank Accession Number AF234296 and
 pTA7002 (Aoyama, T. and Chua N.-H., 1997, Plant J. 11:605-612).
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gene complement(11945..13160)
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DB 93 AATATATATGACACTTATATATGATGCGCTGATPACTAGAACCTATGTAAGAAAAC 152
QY 121 CATCCACTACTTAGTGGCAATCGGGCTAAATATAAGAGTGCCTACA----CTAGTT 176
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QY 177 TCGTTTTCCTTAGTAAATTAAGTGGAAATGAATCATTTATGCTTAGATATACCTTCA 236
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LOCUS			linear
DEFINITION	Sequence 15 from Patent WO2005024029.		PAT 31-MAR-2005
ACCESSION	CS055056		
VERSION	CS055056.1	GI:62121528	
KEYWORDS			
SOURCE			
ORGANISM	Oryza sativa		
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REFERENCE			
AUTHORS	Broekaert, W., Frankard, V., Hatzfeld, Y. and Mironov, V.		
TITLE	Plants having modified growth characteristics and method for making the same		
JOURNAL	Patent: WO 2005024029-A 15 17-MAR-2005;		
FEATURES	CropDesign N.V. (BE)		
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Best Local Similarity	98.9%;	Pred. No. 0;	
Matches 2172; Conservative	0;	Mismatches 18;	Indels 6; Gaps 4;

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Db	121	CATCACCCTACTTTAGTGGCAATGGGGCTAATATAAAAAGGTGCTCACATGTTTGT	180
QY	181	TTTCCCTTAGTATTAAGTGGAAAAATGAAATCATTTATGCTTAGAATATACGTTACATC	240
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QY	778	AAAAAAGAAATTTTGTGCTGTGGGAGGCGCAATCTCCCATATTTGGGACACAGGCA	837
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QY 1920 TGGATTTATTTTATTTATAGCTTTCACCCCTCAATTTCTGAGCTGAAAGCTGAGAG 1979
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RESULT 12
AR643981
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DEFINITION Sequence 50 from patent US 6867293.
ACCESSION AR643981
VERSION AR643981.1 GI:62782641
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 898)
AUTHORS Andrews,C.J., Bachoo,S., Hawkes,T.R., Pickerill,A.P. and Warner,S.A.J.
TITLE polynucleotide constructs having at least one transcriptional enhancer and encoding a modified rice E9PS enzyme
JOURNAL Patent: US 6867293-A 50 15-MAR-2005;
SYNOPSIS Syngetica limited; Guilford;
MOX;

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ORIGIN

Query Match 39.5%; Score 867.2; DB 6; Length 898;
Best Local Similarity 99.2%; Pred. No. 3.9e-147;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

QY 1 AATCGGAAAGTTTCTGACCGTTTCAAGCTCTAATCAATATAGGAAAGTGTGCT 60
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QY 541 AAGGATCTTACGACACACTTTGCTCATGATGATGATGATGATGATGATGAT 599
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QY 600 CGTTCACTAGGACACATCTTCATATCACTGCTTATTAATGATGATGATGAT 659

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RESULT 13

AX044095 898 bp DNA linear PAT 24-NOV-2000
LOCUS AX044095 Sequence 50 from Patent WO0066748.
DEFINITION AX044095
ACCESSION AX044095
VERSION AX044095.1 GI:11342973
KEYWORDS

SOURCE

Oryza sp.
Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and
Plickerill, A.P.
Herbicide resistant plants
Patent: WO 0066748-A 50 09-NOV-2000;
ZENECA LIMITED (GB)

FEATURES

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/mol_type="unassigned DNA"
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Query Match 39.5%; Score 867.2; DB 6; Length 898;
Best Local Similarity 99.2%; Pred. No. 3.9e-147;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

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Db 479 TATTAGTAAATTAAGACATTTGACTTTATTTTATTTATTTTCTTTTGGATTAAGATGC 538
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Db 539 AAGGATCTTAGGACACACTTTTGCTCATATGTCATGTGTAGTGACGACCTCTC-ATAACA 598
Qy 600 CGTTCAACTAGGACACATCTCAATATACATCGGCTATTATATACATTTAGTAGCAAT 659
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Db 839 ACAACAGAGTGCTGCCACAGAACCAACCAAAAAAGATGATCTAAGGAGGACAGC 898

RESULT 14

AX044183 898 bp DNA linear PAT 24-NOV-2000
LOCUS AX044183 Sequence 35 from Patent WO0066746.
DEFINITION AX044183
ACCESSION AX044183
VERSION AX044183.1 GI:11343061
KEYWORDS

SOURCE

Oryza sp.
Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and
Plickerill, A.P.
Herbicide resistant plants
Patent: WO 0066746-A 35 09-NOV-2000;
ZENECA LIMITED (GB)

FEATURES

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/mol_type="unassigned DNA"
/db_xref="taxon:52841"

ORIGIN

Query Match 39.5%; Score 867.2; DB 6; Length 898;
Best Local Similarity 99.2%; Pred. No. 3.9e-147;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

Qy 1 AATCGAAAAGTTTCTGACCGTTTTCACGTCCTAATACTAACAATATAGGAAAGTGTCT 60
Db 2 AATCGAAAAGTTTCTGACCGTTTTCACGTTCTAATACTAACAATATAGGAAAGTGTCT 61
Qy 61 AATAATATAAGACCTTATATATATATAGTACCGCTGATTAAGTATGTAAGAAAAGT 120
Db 62 AATAATATAAGACCTTATATATATATAGTACCGCTGATTAAGTATGTAAGAAAAGT 121

Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,
Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takeku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.

FEATURES

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1..752
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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ORIGIN

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Best Local Similarity 97.2%; Pred. No. 2.2e-12;
Matches 137; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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Oy 1083 GGACCGCCTTCTTCGATCATATCTTCGGTCGAGTTCTTGATCGATCTTCCCTCCTC 1142
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Db 65 GGACCGCC-TCTCGATCCATATCTTCGGTCGAGTTCTTGATCGATCTTCCCTCCTC 123
Oy 1143 CACCTCTCTCTCAGAGGTAT 1163
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Db 124 CACCTCTCTCTCAGAGTTCT 144

Search completed: April 21, 2006, 15:46:39
Job time : 10747 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:53:40 ; Search time 1226 Seconds
(Without alignments)
11932.300 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195
Sequence: 1 aatcgcgaagaattcttcacac.....cacttcaccagcaagttc 2195

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*

1: geneseqn1980a:*

2: geneseqn1990a:*

3: geneseqn2000a:*

4: geneseqn2001a:*

5: geneseqn2001b:*

6: geneseqn2002a:*

7: geneseqn2002b:*

8: geneseqn2003a:*

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10: geneseqn2003c:*

11: geneseqn2003d:*

12: geneseqn2004a:*

13: geneseqn2004b:*

14: geneseqn2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	100.0	2195	13	ADRO1013 Regulator
2	2139.2	97.5	3032	13	ADT92083 PRO129-C
3	2133.4	97.2	9361	3	Ado1285 Rice tran
4	2133.4	97.2	10629	3	Ado1286 Rice tran
5	2115.2	96.4	2191	14	ADY69039
6	867.2	39.5	898	3	AAC88400
7	867.2	39.5	898	3	AAC87195
8	126.8	5.8	719	10	ADK5377
9	126.8	5.8	724	10	ADD16740
10	126.8	5.8	725	10	ADK59227
11	126.8	5.8	782	10	ADD17562
12	126.8	5.8	808	12	ADJ39051 Plant CDN
13	84.6	3.9	2000	11	ACU36783
14	61.2	2.8	2000	11	ACU38652
15	55.6	2.5	101954	13	ABD33574
16	55.4	2.5	8056	8	ABZ10246
17	55.2	2.5	612	14	ACU64894
18	55.2	2.5	5379	6	ABL3676
19	55.2	2.5	5379	6	ABL34576 Human met

20	55.2	2.5	5379	6	ABL70369	Ab170369 Chemical1
21	55.2	2.5	5379	7	ADT99837	Adt99837 Bisulphic
22	55	2.5	69081	11	ACN44642	Acn44642 Human gen
23	54.8	2.5	2482	14	ADZ71091	Adz71091 Human chr
24	54.4	2.5	16766	6	ABJ34156	Abj34156 Human imm
25	53.8	2.5	9760	6	ABK31242	Abk31242 Signal tr
26	53.8	2.5	9760	6	ABL70197	Ab170197 Chemical1
27	53.8	2.5	9760	6	AA61155	Aa61155 Human gen
28	53.8	2.5	47108	6	ABK31511	Abk31511 Signal tr
29	53.6	2.4	700	4	AAH93026	Aah93026 Human inf
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32	53.2	2.4	2501	14	ADY98099	Ady98099 Bisulphic
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41	51.6	2.4	147300	12	ADP45593	Adp45593 Human rho
42	51.6	2.4	147700	14	ADX98570	Adx98570 Human gua
43	51.4	2.3	5979	4	AA645313	Aa645313 Chemical1
44	51.4	2.3	5979	6	ABK28152	Abk28152 DNA trans
45	51.4	2.3	7341	6	ABQ67109	Abq67109 Human ang

ALIGNMENTS

RESULT 1	ADRO1013	standard; DNA; 2195 BP.
ID	ADRO1013	
XX	ADRO1013;	
AC		
XX		
DT	21-OCT-2004 (first entry)	
XX		
DE	Regulatory DNA sequence of the rice GOS2 gene SeqID 1.	
KW	regulatory; plant; rice; GOS2; non-monocotyledonous; transgenic; ds.	
OS	Oryza sativa.	
XX		
PN	WO2004065596-A2.	
XX		
PD	05-AUG-2004.	
XX		
PF	21-JAN-2004; 2004WO-EP000645.	
XX		
PR	21-JAN-2003; 2003BP-00075207.	
XX		
PA	(CROP-) CROPPESIGN NV.	
PI	Hatzfeld Y, Inze D;	
XX		
DR	WPI; 2004-562175/54.	
XX		
PT	Use of a regulatory nucleic acid sequence for driving expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
XX		
PS	Claim 1; SEQ ID NO 1; 25pp; English.	
XX		
CC	This invention relates to a novel isolated regulatory nucleic acid sequence that is useful in the field of plant molecular biology.	
CC	Specifically, it refers to a regulatory gene of the rice GOS2 gene that can drive expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
CC	The present invention describes introducing a regulatory sequence that results in constitutive expression (with levels similar to that of CamV 35S) of an isolated or endogenous nucleic acid sequence in a transgenic non-monocotyledonous plant. In	

CC particular, a plant cell derived from either a fodder or forage legume,
CC ornamental plant, food crop, tree or shrub, preferably from cotton,
CC potato, tomato, cabbage, sugar beet, soybean, sunflower, or peas. This
CC polynucleotide sequence is the regulatory sequence of the rice GOS2 gene
CC of the invention.

XX
SQ Sequence 2195 BP; 639 A; 426 C; 403 G; 727 T; 0 U; 0 Other;

Query Match 100.0%; Score 2195; DB 13; Length 2195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX
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XX
DT 13-JAN-2005 (first entry)
XX
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XX
KM MT2a; plant growth; plant development; transgenic; genetic modification;
KW metallothionein; metal accumulation; abiotic stress; growth regulator;
KM gene; ss.
OS Synthetic.
XX
PN WO2004090142-A2.
XX
PD 21-OCT-2004.
XX
PF 14-APR-2004; 2004WO-EP050519.
XX
PR 14-APR-2003; 2003EP-00076086.
PA (CROP-) CROPDSEIGN NV.
PI Sanz Molinero AI;
XX
DR MPI; 2004-748770/73.
XX
PT Modifying plant growth and development for altering growth
PT characteristics in plants, comprises introducing a genetic modification
PT in the plant and selecting modulated expression of a nucleic acid
PT encoding a metallothionein protein.
XX
PS Claim 13; SEQ ID NO 7; 49pp; English.
XX
CC The invention relates to modifying plant growth and development and
CC involves introducing a genetic modification in the plant and selecting
CC for modulated expression in the plant of a nucleic acid encoding a
CC metallothionein protein, provided that the modified growth and
CC development is not increased metal accumulation or increased tolerance or
CC resistance to abiotic stress. In modifying plant growth and development,
CC the modified plant growth and development is increased yield, preferably
CC an increase of biomass and/or seed yield, when compared to corresponding
CC wild type plants. Genetic modification comprises introducing an isolated
CC nucleic acid encoding a metallothionein protein into a plant. The nucleic
CC acid encoding a metallothionein protein encodes a type 2 metallothionein
CC and is derived from a plant, preferably a dicotyledonous plant, more
CC preferably from the family Brassicaceae, e.g. Arabidopsis thaliana. The
CC expression of the nucleic acid encoding a metallothionein is driven by a
CC constitutive promoter, preferably the rice GOS2 promoter. The
CC metallothionein protein and its homologues, derivatives, and active
CC fragments, and the encoding polynucleotides are useful for modifying the
CC growth characteristics of plants, provided that the modified growth and
CC development is not increased metal accumulation or increased tolerance or
CC resistance to abiotic stress. They are also useful as a growth regulator.
CC The method is useful for modifying plant growth and development. It is

CC also useful for producing plants with altered growth characteristics,
CC e.g. increased yield, increased biomass, increased total above ground
CC area, increased plant height, increased number of tillers, increased
CC number of primary panicles, increased total number of seeds, or increased
CC harvest index. The present sequence represents the nucleotide sequence of
CC an FRO0129-CDS1585 -zein and IBCS delta8A double terminator expression
CC cassette for the expression of A. thaliana AtMT2a gene.
XX
SQ Sequence 3032 BP; 917 A; 595 C; 581 G; 939 T; 0 U; 0 Other;
Query Match 97.5%; Score 2139.2; DB 13; Length 3032;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 2174; Conservative 0; Mismatches 18; Indels 4; Gaps 2;
QY 1 AATCGAAAAAGTTTCTGACCGTTTTCACGTCCTTAATACAAATATAGGAAACGTGTCT 60
DB 1 AATCGAAAAAGTTTCTGACCGTTTTCACCGCTTAATACAAATATAGGAAACGTGTCT 60
QY 61 AATATATAAATGAGACCTTAATATATATAGCCGTGATTAATAGAACTATGTAAGAAAACT 120
DB 61 AATATATAAATGAGACCTTAATATATATAGCCGTGATTAATAGAACTATGTAAGAAAACT 120
QY 121 CATCCACTACTTTAGTGGCAATCGGCTAAATTAAGAGTGGCTACACTAGTTTGT 180
DB 121 CATCCACTACTTTAGTGGCAATCGGCTAAATTAAGAGTGGCTACACTAGTTTGT 180
QY 181 TTTCTTGTATTAATGAGGAAATGAATCATTTGCTTGAATATAGCTTACATC 240
DB 181 TTTCTTGTATTAATGAGGAAATGAATCATTTGCTTGAATATAGCTTACATC 240
QY 241 TCTGTATGAAATTAATTAATTCGAGTATGATTAATGATCAATCTTTCTTGAATA 300
DB 241 TCTGTATGAAATTAATTAATTCGAGTATGATTAATGATCAATCTTTCTTGAATA 300
QY 301 AAAAAATCTTTCTAGCTGAATCAATGGTAAAGAAATTTTTTTTAAAAAAAT 360
DB 301 AAAAAATCTTTCTAGCTGAATCAATGGTAAAGAAATTTTTTTTAAAAAAAT 360
QY 361 AGAATGAATATTTCTGAACGATATGCGAAAGATTTAAACATTAATTAATTAATTTAT 420
DB 361 AGAATGAATATTTCTGAACGATATGCGAAAGATTTAAACATTAATTAATTAATTTAT 420
QY 421 AGTTGTGCAATTCGTAATATGCGACGTCATTAAGGACATGCTTAACTCAATCTCAATTT 480
DB 421 AGTTGTGCAATTCGTAATATGCGACGTCATTAAGGACATGCTTAACTCAATCTCAATTT 480
QY 481 TATTTAGTAATTAAGAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 540
DB 481 TATTTAGTAATTAAGAAATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 540
QY 541 AAGGTAATTAAGCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 599
DB 541 AAGGTAATTAAGCAACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 599
QY 600 CGTTCACTAGGCAACATTCATATATCACTGCGCTTAATTAATCAATTTAGTAGCAAT 659
DB 600 CGTTCACTAGGCAACATTCATATATCACTGCGCTTAATTAATCAATTTAGTAGCAAT 659
QY 658 ATCTGAATTCAGCACTTCAACATCAACGACCACTTTTAATTAATTAATTAATTAATTAAT 717
DB 658 ATCTGAATTCAGCACTTCAACATCAACGACCACTTTTAATTAATTAATTAATTAATTAAT 717
QY 720 AATATTTTACAGATAGATGAAGAAATGATGAAGAAATGATGAAGAAATGATGAAGAAATG 779
DB 720 AATATTTTACAGATAGATGAAGAAATGATGAAGAAATGATGAAGAAATGATGAAGAAATG 779
QY 778 AAAAAAAGAAATTTTCTGTCGTCGAGGCGCAATCTCCATATTTGGGACACAGGCA 839
DB 778 AAAAAAAGAAATTTTCTGTCGTCGAGGCGCAATCTCCATATTTGGGACACAGGCA 839
QY 840 ACAACAGATGCTGCCACAGAACACCAACCAAAACAAATGATCTTAACGAGAGACAGC 899
DB 840 ACAACAGATGCTGCCACAGAACACCAACCAAAACAAATGATCTTAACGAGAGACAGC 899
QY 897 ACAAAGATGCTGCCACAGAACACCAACCAAAACAAATGATCTTAACGAGAGACAGC 897

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QY 900 AAGTCGCAACAACCTTTTAAAGCAGAGCTTTCGCGCCAGAGAGAGAGAGAGAGCANA 959
DB 898 AAGTCGCAACAACCTTTTAAAGCAGAGCTTTCGCGCCAGAGAGAGAGAGAGAGCANA 957
QY 960 GAAAAACAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1019
DB 958 GAAAAACAAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1017
QY 1020 ATAGAGGAGCATCAAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079
DB 1018 ATAGAGGAGCATCAAGCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
QY 1080 GAGCGACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1139
DB 1078 GAGCGACCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1137
QY 1140 CTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1199
DB 1138 CTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1197
QY 1200 TTGTGATGACGGGGCGGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259
DB 1198 TTGTGATGACGGGGCGGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1257
QY 1260 TTGGAATTTGGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1319
DB 1258 TTGGAATTTGGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1317
QY 1320 TATGCTTTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1379
DB 1318 TATGCTTTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1377
QY 1380 TGCAGATTTGTGATGATCTTTTGTGATGATCTTTGATGATCTTTGATGATCTTTGAT 1439
DB 1378 TGCAGATTTGTGATGATCTTTTGTGATGATCTTTGATGATCTTTGATGATCTTTGAT 1437
QY 1440 TGTAAATAAAGATGATCTTTTGTGATGATCTTTGATGATCTTTGATGATCTTTGATG 1499
DB 1438 TGTAAATAAAGATGATCTTTTGTGATGATCTTTGATGATCTTTGATGATCTTTGATG 1497
QY 1500 AAGCTATCTTTGTTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1559
DB 1498 AAGCTATCTTTGTTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1557
QY 1560 TTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1619
DB 1558 TTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1617
QY 1620 GATACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1679
DB 1618 GATACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
QY 1680 TTCCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1739
DB 1678 TTCCCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1737
QY 1740 TCACCTTTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1799
DB 1738 TCACCTTTCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1797
QY 1800 CTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1859
DB 1798 CTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1857
QY 1860 CGATTTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1919
DB 1858 CGATTTCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1917
QY 1920 TGGATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1979
DB 1918 TGGATTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1977

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QY 1980 AACTGCTCAATTTGTTTCAAAATTCATTCGATTTATTCGATTTATCTCTGTTAT 2039
DB 1978 AACTGCTCAATTTGTTTCAAAATTCATTCGATTTATTCGATTTATCTCTGTTAT 2037
QY 2040 CTACCTGATGAGATTTCTTTTGGTATTCCTGTGACGCTGATTTACGAGAAAGAAATTTA 2099
DB 2038 CTACCTGATGAGATTTCTTTTGGTATTCCTGTGACGCTGATTTACGAGAAAGAAATTTA 2097
QY 2100 TGAAGCTGTAATCGGATGATGATTAATCTGCTGTTATGATGATTAATTTCTTTTGACAGT 2159
DB 2098 TGAAGCTGTAATCGGATGATGATTAATCTGCTGTTATGATGATTAATTTCTTTTGACAGT 2157
QY 2160 TCTTGCTGATGCTGCCACTTTACACAGCAAAAGTTTC 2195
DB 2158 TCTTGCTGATGCTGCCACTTTACACAGCAAAAGTTTC 2193

RESULT 3
AAd01285/c
ID AAd01285 standard; DNA; 9361 BP.
AC AAd01285;
XX
XX
DT 12-OCT-2000 (first entry)
XX
DB Rice transformation vector; pGOS2-hpc.
XX
XX Matrix Attachment Region; MAR; rice transformation vector; pGOS2-hpc;
KW scaffold attachment region; gene expression; transgenic organism; de.
XX
XX Synthetic.
OS
XX
XX WO20032800-A1.
PN
XX
XX 08-JUN-2000.
PD
XX
XX 30-NOV-1999; 99WO-US028123.
PF
XX
XX 01-DEC-1998; 98US-0110437P.
PR
XX
XX (IDWC ) DOM AGROSCIENCES LLC.
PA
XX
XX Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;
PI
XX
XX WPI; 2000-412345/35.
DR
XX
XX An isolated DNA molecule for use as a matrix attachment region to
PT increase expression of genes introduced in transformed plants comprises a
PT 298 base pair sequence described in the specification.
XX
XX
XX Example 3; Page 48-51; 73pp; English.
XX
XX The patent discloses a DNA molecule, useful as matrix attachment region
CC (MAR) or scaffold attachment region, to increase the expression of genes
CC introduced in transformed plants. MARs are located in non-transcribed
CC regions of genes and form the physical boundaries of individual DNA
CC loops. They are rich in adenosine and thymine bases and contain certain
CC conserved sequence elements and structural features. They are about 300-
CC 2000 bp in length. Increased levels of expression of DNA introduced into
CC plants can be achieved by use of MAR. They can also reduce the position
CC effect in transgenic organisms. The present DNA sequence is the rice
CC transformation vector pGOS2-hpc, that contains a hygromycin selectable
CC marker driven by the 35S promoter and a GOS2/GUS/nos cassette (GOS2
CC transcripion initiation region/GUS structural gene/nos 3' untranslated
CC region). The GOS2 transcripion initiation region in this construct is
CC comprised of 1010 bp of promoter and 170 bp of untranslated 5' leader
CC interrupted by a 1100 bp intron sequence
XX
XX
XX Sequence 9361 BP; 2449 A; 2285 C; 2190 G; 2435 T; 0 U; 2 Other;
SQ

Query Match 97.2%; Score 2133.4; DB 3; Length 9361;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2167; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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QY	10	AGTTTCGACCCGTTTTCAGCTCCTTAACATAATATAGGGAAGCTGTGCTAAATATATAA	69
Db	7083	AGTTTCGACCCGTTTTCACCCCTTAACATAATATAGGGAAGCTGTGCTAAATATATAA	7024
QY	70	ATGAGACCTTATATATGTAGGCGTATATACTAGAACTATGTATAGAAAAAATCATCCACT	129
Db	7023	ATGAGACCTTATATATGTAGGCGTATATACCTAGAACTATGTAGAAAAAATCATCCACT	6964
QY	130	ACTTATAGGCAATCGGGCTAAATTAATAAAGATCGCTACACTAGTTCGTTTTCTTAG	189
Db	6963	ACTTATAGGCAATCGGGCTAAATTAATAAAGATCGCTACACTAGTTCGTTTTCTTAG	6904
QY	190	TAAATTAAGTGGAAAAATGAATCATTAATGCTTATAGATATATACGTTCAATCTGTCAATG	249
Db	6903	TAAATTAAGTGGAAAAATGAATCATTAATGCTTATAGATATATACGTTCAATCTGTCAATG	6844
QY	250	AAGTTAATTAATTCGAGGTAGCCATAATTTGTCATCAAACTCTTCTGTAGTAAATAAATCT	309
Db	6843	AAGTTAATTAATTCGAGGTAGCCATAATTTGTCATCAAACTCTTCTGTAGTAAATAAATCT	6784
QY	310	TTCTTAGCTGAATCTCAATGGGTAAAGAGATATTTTTTTTAAAAAAAATATAGATAG	369
Db	6783	TTCTTAGCTGAATCTCAATGGGTAAAGAGATATTTTTTTT---AAAAAATAGATAG	6727
QY	370	ATATTCTGAACGTATCGGCAAAAGATTTTAACATAATAATTATATATATTAATGTTGTGC	429
Db	6726	ATATTCTGAACGTATTTGGCAAAAGATTTTAACATAATAATTATATATATTAATGTTGTGC	6667
QY	430	ATTGCTTATTCGACCGTCATTTAAGAGATGTCTTACCTCAATTTTATTTATTTAGTA	489
Db	6666	ATTGCTTATTCGACCATTTAAGAGATGTCTTACCTCAATTTTATTTATTTAGTA	6607
QY	490	ATTAAAGACAATTTGACTTAATTTTATATTTATCTTTTTCGATTAGTGCAGAGTACTT	549
Db	6606	ATTAAAGACAATTTGACTTAATTTTATATTTATCTTTTTCGATTAGTGCAGAGTACTT	6547
QY	550	AAGCACAACATTTGTGCTCATGTGATGTGATGTCACCTCTC-ATACACGTTCACT	608
Db	6546	AAGCACAACATTTGTGCTCATGTGATGTGATGTCACCTCTCAATACACGTTCACT	6487
QY	609	AGCGACATCTCCAAATATCACTGTGCTTATTTAATCACTTTAGTAGCAATATCTGAATT	668
Db	6486	AGCAACATCTCTAATATCACTGTGCTTATTTAATCACTTTAGTAGCAATATCTGAATT	6427
QY	669	CAAGACCTTCAACATCAACAGACCACTTTAATAATATCTAAATATCAAAAATAATTTT	728
Db	6426	CAAGACCTTCAACATCAACAGACCACTTTAATAATATCTAAATATCAAAAATAATTTT	6367
QY	729	ACAGAAATAGCAAAAAATATGAACGAATCTATTAGGTTTTTTCACATACAAAAAATAA	788
Db	6366	ACAGAAATAGCAAAAAATATGAACGAATCTATTAGGTTTTTTCACATACAAAAAATAA	6307
QY	789	AGAAATTTTGTCTGTGCGGAGCGCCCAATCTCCATATTGGGACACAGGCAACAAGAG	848
Db	6306	AGAAATTTTGTCTGTGCGGAGCGCCCAATCTCCATATTGGGACACAGGCAACAAGAG	6247
QY	849	TGCGTGTGCCACAGAACCAACCAAAAAACATATCTAACAGAGAGACAGAAATCTCGCA	908
Db	6246	TGCGTGTGCCACAGAACCAACCAAAAAACATATCTAACAGAGAGACAGAAATCTCGCA	6187
QY	909	ACAACCTTTTAAACAGCAGGCTTTGGCGGCAGAGAGAGAGAGAGAGCAAGCAAAACAA	968
Db	6186	ACAACCTTTTAAACAGCAGGCTTTGGCGGCAGAGAGAGAGAGAGAGCAAGCAAAACAA	6127
QY	969	GCATCTCTCTCTCCCATCTATAAATTCCTCCCTTTTCCCTCTCTATATAGAGGC	1028
Db	6126	GCATCTCTCTCTCCCATCTATAAATTCCTCCCTTTTCCCTCTCTATATAGAGGC	6067
QY	1029	ATCCAGCGCAAGAGAGGAGAGACCAAGACACGCACTTAGCAAGAAAGCCGACGACCG	1088
Db	6066	ATCCAGCGCAAGAGAGGAGAGACCAAGACACGCACTTAGCAAGAAAGCCGACGACCG	6007

QY	1089	CCCTTCCTGCATCCATATCTCCGGTCCAGTCTTGCGCATCTCTCCCTCCACCTC	1148
Db	6006	CCCTTCCTGCATCCATATCTCCGGTCCAGTCTTGCGCATCTCTCCCTCCACCTC	5947
QY	1149	CTCCTCACAGGGATATGTCGCTTCGGTGTCTTGATTTATATTTGTCAGGTGTGTAGT	1208
Db	5946	CTCCTCACAGGGATATGTCGCTTCGGTGTCTTGATTTATATTTGTCAGGTGTGTAGT	5887
QY	1209	ACGGGCGTGTGATGTAGAAAAGGGGATCTGTATCTGTGATGATTTCTGTTCCTTGAAATTTG	1268
Db	5886	ACGGGCGTGTGATGTAGAAAAGGGGATCTGTATCTGTGATGATTTCTGTTCCTTGAAATTTG	5827
QY	1289	GGATATGAGGGGTCCTTGATCTTGATCTGTATCCGTCCTGGTTTGATTTAGTATGATGTTTT	1328
Db	5826	GGATATGAGGGGTCCTTGATCTTGATCTGTATCCGTCCTGGTTTGATTTAGTATGATGTTTT	5767
QY	1329	CAATCGTCGTGAGAGCTCTATGAGAAATGAAATGCTTTAGGGTACGGAACTTTCGCAATTTT	1388
Db	5766	CAATCGTCGTGAGAGCTCTATGAGAAATGAAATGCTTTAGGGTACGGAACTTTCGCAATTTT	5707
QY	1389	GTGAGTACCTTTTGTGAGGTAAATCAGAGCACGGGTGATTTTGTGTGTATATAA	1448
Db	5706	GTGAGTACCTTTTGTGAGGTAAATCAGAGCACGGGTGATTTTGTGTGTATATAA	5647
QY	1449	AGTACATTTGTTTGTCCTCGATTCCTGTAGTATGCTTCTCCATTTGAGAGACTATCC	1508
Db	5646	AGTACATTTGTTTGTCCTCGATTCCTGTAGTATGCTTCTCCATTTGAGAGACTATCC	5587
QY	1509	TTTGTTTATTCCTCATTTGAAACAAAATATATCACTTTGAAAGAGCGTCCGTTGATGAGA	1568
Db	5586	TTTGTTTATTCCTCATTTGAAACAAAATATATCACTTTGAAAGAGCGTCCGTTGATGAGA	5527
QY	1569	TTGATATGATTGATCTTAAAGCTGTGCCAAATTTTCGAGCTGCTGCTTTTATGATACAGTA	1628
Db	5526	TTGATATGATTGATCTTAAAGCTGTGCCAAATTTTCGAGCTGCTGCTTTTATGATACAGTA	5467
QY	1629	GTCCCATCACGAAATTCATGAAAAAGTTTAACTCTCAGAGACAGGGGATTCCTGCTT	1688
Db	5466	GTCCCATCACGAAATTCATGAAAAAGTTTAACTCTCAGAGACAGGGGATTCCTGCTT	5407
QY	1689	CTTCGATTTGCTTTAGTCCGAGAAATTTTTTCCCAAATATCTTAAAGTCACTTTCCT	1748
Db	5406	CTTCGATTTGCTTTAGTCCGAGAAATTTTTTCCCAAATATCTTAAAGTCACTTTCCT	5347
QY	1749	GGTTCAGTTCATGAAATTTGTCGTACAAATATGCTTTTATATAGCGTTATCCTAGCTGTA	1808
Db	5346	GGTTCAGTTCATGAAATTTGTCGTACAAATATGCTTTTATATAGCGTTATCCTAGCTGTA	5287
QY	1809	GTTCAAGTTTATAGGTAAATCCCTATATAGTTAGTCAGAGAGAGAACTTATCCGATTTCTG	1868
Db	5286	GTTCAAGTTTATAGGTAAATCCCTATATAGTTAGTCAGAGAGAGAACTTATCCGATTTCTG	5227
QY	1869	ATCTCCATTTTAAATATATATGAAATGAACTGTAGACATTAAGACAGTATCATTTGGATTAAT	1928
Db	5226	ATCTCCATTTTAAATATATATGAAATGAACTGTAGACATTAAGACAGTATCATTTGGATTAAT	5167
QY	1929	TTTTTAAATAGCTTACCCCTCATTAATTCGAGCTGAAAGTGTGGCATGAACTGTCTCT	1988
Db	5166	TTTTTAAATAGCTTACCCCTCATTAATTCGAGCTGAAAGTGTGGCATGAACTGTCTCTCT	5107
QY	1989	CAATTTGTATTCAAAATTCACATGATTAATCTATGATATCTCTTGTATCTACCTGTA	2048
Db	5106	CAATTTGTATTCAAAATTCACATGATTAATCTATGATATCTCTTGTATCTACCTGTA	5047
QY	2049	GAAATTTCTTTTGGTATATCTCTGACCTGTGATTAAGAAAAGAAATTTATGAAAGCTGT	2108
Db	5046	GAAATTTCTTTTGGTATATCTCTGACCTGTGATTAAGAAAAGAAATTTATGAAAGCTGT	4987
QY	2109	AATGGGAGTATATATACGCTGTTCTTATGATTAATTCCTTTGTGTCAGTCTTGGTGT	2168
Db	4986	AATGGGAGTATATATACGCTGTTCTTATGATTAATTCCTTTGTGTCAGTCTTGGTGT	4927
QY	2169	AGCTTGCCACTTTCACGACAAAGTTC	2195

|||||
DB 4926 AGCTTGCCACTTTCACGACGAAAGTTC 4900
RESULT 4
AAD01286/c
ID AAD01286 standard; DNA; 10629 BP.
XX AAD01286;
AC
XX
XX
DT 12-OCT-2000 (first entry)
DE Rice transformation vector, pARGOS2AF-hpt.
XX
XX Matrix Attachment Region; MAR; rice transformation vector; pARGOS2AF-hpt;
KM scaffold attachment region; gene expression; transgenic organism; de.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 2735..3389
FT /tag= a
FT /note= "Corresponds to nucleotides 14-668 of MAR dimer-2"
FT misc_feature 7730..8384
FT /tag= b
FT /note= "Corresponds to nucleotides 1-655 of MAR dimer-1"
XX
XX WO20032800-A1.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028123.
XX
XX 01-DEC-1998; 98US-0110437P.
XX
XX (DOMC) DOM AGRSCIENCES LLC.
XX
XX Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;
XX
XX WPI; 2000-412345/35.
XX
XX An isolated DNA molecule for use as a matrix attachment region to
PT increase expression of genes introduced in transformed plants comprises a
FT 298 base pair sequence described in the specification.
XX
XX
XX PS Example 3; Page 51-54; 73pp; English.
XX
XX The patent discloses a DNA molecule, useful as matrix attachment region
CC (MAR) or scaffold attachment region, to increase the expression of genes
CC introduced in transformed plants. MARs are located in non-transcribed
CC regions of genes and form the physical boundaries of individual DNA
CC loops. They are rich in adenosine and thymine bases and contain certain
CC conserved sequence elements and structural features. They are about 300-
CC 2000 bp in length. Increased levels of expression of DNA introduced into
CC plants can be achieved by use of MAR. They can also reduce the position
CC effect in transgenic organisms. The present DNA sequence is the rice
CC transformation vector pARGOS2AF-hpt, identical to the vector pGOS2-
CC except that it contains a MAR dimer-2 positioned 5' to the GOS2
CC transcription initiation region and the MAR dimer-1 positioned 3' to the
CC nos 3' UTR (untranslated region). This vector is used to efficiently
CC transform monocot plants like rice
XX
XX Sequence 10629 BP; 2904 A; 2469 C; 2369 G; 2887 T; 0 U; 0 Other;
SQ
Query Match 97.2%; Score 2133.4; DB 3; Length 10629;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2167; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
QY 10 AGTTTCGACCGCTTTTACGTCCTAACATAATATAGGAACGTCGCTAAATATAA 69
DB 7722 AGTTTCGACCGCTTTTACCGCTTAACATAATATAGGAACGTCGCTAAATATAA 7663
QY 70 ATGAGACCTTAATATATGAGCGCTGATTAAGAACTATGTAAGAAAACTCATCCACCT 129

|||||
DB 7662 ATGAGACCTTAATATATGAGCGCTGATTAAGAACTATGTAAGAAAACTCATCCACCT 7603
QY 130 ACTTAGTGGAATCGGCTAAATTAATAAGATCGTACACTAGTTTCGTTTCCTTAG 189
DB 7602 ACTTAGTGGAATCGGCTAAATTAATAAGATCGTACACTAGTTTCGTTTCCTTAG 7543
QY 190 TAATTAAGTGGAAAAATGAATCATTAATGCTTGAATATAGTTACATCTCTGTCAATG 249
DB 7542 TAATTAAGTGGAAAAATGAATCATTAATGCTTGAATATAGTTACATCTCTGTCAATG 7483
QY 250 AAGTTAAATTAATGAGGTACCAATTAATGTCATCAACCTCTCTGAAATTAATAAATCT 309
DB 7482 AAGTTAAATTAATGAGGTACCAATTAATGTCATCAACCTCTCTGAAATTAATAAATCT 7423
QY 310 TTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTTTAAAAAAAATAGATGAG 369
DB 7422 TTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTTT---AAAAAATAGATGAG 7366
QY 370 ATATTCTGAAACGTATCGGCAAGAATTTAAACATATTAATATATATATATATGTTGTGC 429
DB 7365 ATATTCTGAAACGTATCGGCAAGAATTTAAACATATTAATATATATATATATGTTGTGC 7306
QY 430 ATTGCTTATATGCAACGCTATTAAGAGACATGCTTACCTCCATCTCCATTTTATTTAGTA 489
DB 7305 ATTGCTTATATGCAACATTAAGAGACATGCTTACCTCCATCTCCATTTTATTTAGTA 7246
QY 490 ATTAAGAACAATGACTATATTTTATTTATTTATCTTTTTCGATAGTCAAGATCTT 549
DB 7245 ATTAAGAACAATGACTATATTTTATTTATTTATTTATCTTTTTCGATAGTCAAGATCTT 7186
QY 550 ACGCACACATTTGTGCTCATGTGCATGTGTGAGTGCACCTCTC-ATACAGTTCAACT 608
DB 7185 ACGCACACATTTGTGCTCATGTGCATGTGTGAGTGCACCTCTC-ATACAGTTCAACT 7126
QY 609 AGCGACATCTCCAAATATCACTGGCCATTTAATATCACTTAGTAGCAATATCTGAATT 668
DB 7125 AGCAACATCTCTCAATATATCACTGGCCATTTAATATCACTTAGTAGCAATATCTGAATT 7066
QY 669 CAAGCACTTCAACATCAACGACCACTTTTAAATATCTAAATATCAAAAAATTAATTTT 728
DB 7065 CAAGCACTTCAACATCAACGACCACTTTTAAATATCTAAATATCAAAAAATTAATTTT 7006
QY 729 ACAGAAATGACATGAAGATGAAGCAAGCACTATTAGTTTTCATCATCAAAAAA 788
DB 7005 ACAGAAATGACATGAAGATGAAGCAAGCACTATTAGTTTTCATCATCAAAAAA 6946
QY 789 AGAATTTTGTCTGCGGCGGAGCGCAATCTCCCATTTTGGGCAACAGGCAACAGAG 848
DB 6945 AGAATTTTGTCTGCGGCGGAGCGCAATCTCCCATTTTGGGCAACAGGCAACAGAG 6886
QY 849 TGGTGCCCAAGAACCAACCAAAAAACGATGATCTTAACGAGGACAGCAAGTCCGCA 908
DB 6885 TGGTGCCCAAGAACCAACCAAAAAACGATGATCTTAACGAGGACAGCAAGTCCGCA 6826
QY 909 ACAACCTTTTAAACGACGAGCTTTTCCGCGCAGAGAGAGAGAGGCAAAAGAAACCA 968
DB 6825 ACAACCTTTTAAACGACGAGCTTTTCCGCGCAGAGAGAGAGAGGCAAAAGAAACCA 6766
QY 969 GCATCTCTCTCTCCCATCTTAATATCTCTCTCTCTCTCTCTCTCTCTATATAGAGGC 1028
DB 6765 GCATCTCTCTCTCCCATCTTAATATCTCTCTCTCTCTCTCTCTCTCTATATAGAGGC 6706
QY 1029 ATCCAGGCAAGAGAGAGAGAGACCAAGACAGCAAGCACTAGAGAGAGCCGAGCCG 1088
DB 6705 ATCCAGGCAAGAGAGAGAGAGACCAAGACAGCAAGCACTAGAGAGAGCCGAGCCG 6646
QY 1089 CTTTCTTGATCATATCTCTCGGTGAGTCTTGTGATCTCTTCCCTCCACCTC 1148
DB 6645 CTTTCTTGATCATATCTCTCGGTGAGTCTTGTGATCTCTTCCCTCCACCTC 6586
QY 1149 CTCTCAGAGGATATGTCCTTGGTTGTTCTTGATTTATTTCTAGGTTGTGATG 1208

degenerate as a result of the genetic code, (v) allelic variants of (i) to (iv), where the allelic variant encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, or (vi) alternative splice variants of nucleic acids of (i) to (iv), where the alternative splice variants encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure; and a CDK mutant comprising (i) an amino acid sequence of SEQ ID NOS: 9-13, or (ii) a fragment of SEQ ID NOS: 9-13 where the fragment comprises at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure. Preferred Method: Increasing expression is effected by introducing and expressing in a plant a B-type CDK nucleic acid. The B-type CDK is derived from a plant, algal, or fungal source. The B-type CDK derived from a plant is from a dicotyledonous plant, preferably from the family Brassicaceae, specifically Arabidopsis thaliana. The B-type CDK is a class 1 B-type CDK, preferably a CDK B1,1 or CDK B1,2 from A. thaliana. The B-type CDK is a class 2 B-type CDK, preferably a CDK B2,2 from A. thaliana. The CDK B1,1 nucleic acid comprises a sequence of 930 bp (SEQ ID NO: 1), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 1, and where the CDK B1,1 protein comprises a sequence of SEQ ID NO: 2 or its homologue, derivative or active fragment. The CDK B1,2 nucleic acid comprises a sequence of 946 bp (SEQ ID NO: 3), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 3, and where the CDK B1,2 protein comprises a sequence of SEQ ID NO: 4 or its homologue, derivative or active fragment. The CDK B2,2 nucleic acid comprises a sequence of 948 bp (SEQ ID NO: 5), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 5, and where the CDK B2,2 protein comprises a sequence of SEQ ID NO: 6 or its homologue, derivative or active fragment. The B-type CDK is a variant nucleic acid or variant amino acid, e.g. functional portions of, sequences capable of hybridizing to, alternative splice variants of, or allelic variants of a B-type CDK nucleic acid/gene, homologues, derivatives, or active fragments of a B-type CDK protein, or mutant B-type CDKs. The expression of the CDK B1,1 nucleic acid is driven by a promoter active in young, expanding tissue, preferably where the promoter is beta expansin promoter. The expression of CDK B1,2 nucleic acid CDK B2,2 nucleic acid is driven by a constitutive promoter, specifically a GGS 2 promoter. The increased yield comprises increase in area, increase in the number of panicles, increased in height, increase in the number of seeds, increase in the number of filled seed, increase in total weight of seeds, increase in thousand kernel weight (TKW), or an increase in harvest index, each relative to control plants. The modified architecture includes increase in aboveground area, increase in the number of panicles or increase in height. Producing transgenic plant having improved growth characteristics, e.g. increased yield, increased growth rate, or modified architecture, which growth characteristics are improved relative to growth characteristics of corresponding wild type plants, comprises introducing into a plant or a plant cell a B-type CDK gene/nucleic, or a nucleic acid encoding a CDK mutant comprising at least one of the 7 amino acid position changes listed in the disclosure, and culturing the plant cell under conditions promoting regeneration and mature plant growth. Identifying mutant plant CDKs having enhanced CDK activity relative to corresponding non-mutated plant CDKs comprises providing plant-derived CDK mutants, identifying cyclin dependent kinase inhibitor (ICK) non reacting mutants, identifying mutants having cyclin-binding activity, and optionally a yeast complementation assay on resultant mutants. Identifying substantially non-active plant CDKs, but are capable of binding to plant ICKs, comprises providing plant-derived CDK mutants, identifying plant-derived ICK binding mutants, and identifying non-cyclin binding mutants. The CDK mutants are provided by providing a wild type plant CDK and mutating the CDK at least 1 amino acid position. Preferred Transgenic Plant: The plant is a monocotyledonous plant. The CDK B-type nucleic or CDK B-type amino acid is useful for improving the growth characteristics of a plant, the growth characteristics is increased yield, increased growth rate, or modified architecture (claimed).

Sequence 2191 BP; 638 A; 431 C; 403 G; 719 T; 0 U; 0 Other;

Query Match	96.4%	Score 215.2;	DB 14;	Length 2191;
Best Local Similarity	98.9%;	Pred. No. 0;		
Matches 2172; Conservative	0;	Mismatches 18;	Indels 6;	Gaps 4;

QY	1	AATCGGAAAATTTCTGACCGGTTTTCAAGCTCCATCACTAAATATGAGGAAACGTGGCT	60
Db	1	AATCGGAAAATTTCTGACCGGTTTTCAAGCTCCATCACTAAATATGAGGAAACGTGGCT	60
QY	61	AAATATATAAATGAGACCTTATATATGTATGCGCTGATATACTAGAACTATGTAAAGAAAAC	120
Db	61	AAATATATAAATGAGACCTTATATATGTATGCGCTGATATACTAGAACTATGTAAAGAAAAC	120
QY	121	CATCCACTTACTTTATGTGGCAATGGGGCTAAATAAAAAGGTGGCTACACTAGTTTGGT	180
Db	121	CATCCACTTACTTTATGTGGCAATGGGGCTAAATAAAAAGGTGGCTACACTAGTTTGGT	180
QY	181	TTTCCCTTAGTAATTAAGTGGGAAAATGAAATCATTAATGCTTAGAATATACGTTACATC	240
Db	181	TTTCCCTTAGTAATTAAGTGGGAAAATGAAATCATTAATGCTTAGAATATACGTTACATC	240
QY	241	TCTGTCATGAAGTTAAATTAATTCGAGGTGACCATTAATGTCATCAAACTCTCTTGTGAATA	300
Db	241	TCTGTCATGAAGTTAAATTAATTCGAGGTGACCATTAATGTCATCAAACTCTCTTGTGAATA	300
QY	301	AAAAAATTTTCTTAGCTGCACTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAAAT	360
Db	301	AAAAAATTTTCTTAGCTGCACTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAAAT	360
QY	361	AGAAATGAAGATATTTCTGAAAGCTATTCGGCAAGATTTAAACATATATATATTAATTTTAT	420
Db	358	AGAAATGAAGATATTTCTGAAAGCTATTCGGCAAGATTTAAACATATATATATTAATTTTAT	417
QY	421	AGTTTGTGCATCGTTATATGTGCACGTCTTAATAGGACATGCTCTTACCTCATCTTATTT	480
Db	418	AGTTTGTGCATCGTTATATGTGCACATCTTAATAGGACATGCTCTTACCTCAATCTTATTT	477
QY	481	TATTTAGTAATTAAGAACAATTGACTTAATTTTATTTATTTATCTTTTTCATTAGATGC	540
Db	478	TATTTAGTAATTAAGAACAATTGACTTAATTTTATTTATTTATCTTTTTCATTAGATGC	537
QY	541	AAGGTACTTACGACACACTTTGTGCTCATGTGTCATGTGTAGTGCACCTTCCTC - ATACA	599
Db	538	AAGGTACTTACGACACACTTTGTGCTCATGTGTCATGTGTAGTGCACCTTCCTCAATACA	597
QY	600	CGTTCAACTAGCGACACATCTCCAAATATCACTGGCCTATTTAATACATTTAGATAGCAAT	659
Db	598	CGTTCAACTAGCGACACATCTCTAATATCACTGGCCTATTTAATACATTTAGATAGCAAT	657
QY	660	ATCTGAATTCAGAGACTTCACATCACACAGACACTTTTAATATATCTAAATATACAAA	719
Db	658	ATCTGAATTCAGAGACTTCACATCACACAGACACTTTTAATATATCTAAATATACAAA	717
QY	720	AATATATTTACAGAAATAGCATGAAAGATATGAAACGAATATTTAGGTTTTTCACATACA	779
Db	718	AATATATTTACAGAAATAGCATGAAAGATATGAAACGAATATTTAGGTTTTTCACATACA	777
QY	780	AAAAAATTTTGTGCTGTGCGGAGGCGCAATCTCCCATATTTGGGACACAGGCA	839
Db	778	AAAAAATTTTGTGCTGTGCGGAGGCGCAATCTCCCATATTTGGGACACAGGCA	837
QY	840	ACAAACAGAGTGGCTGCCACAGAACAACCCACAAAACGATGATCTTAACGAGAGACAGC	899
Db	838	ACAAACAGAGTGGCTGCCACAGAACAACCCACAAAACGATGATCTTAACGAGAGACAGC	897
QY	900	AAGTCCGGAACAACCTTTTAAACACAGGCTTTGGCGCAAGAGAGAGAGAGAGGCAAA	959
Db	898	AAGTCCGGAACAACCTTTTAAACACAGGCTTTGGCGCAAGAGAGAGAGAGAGGCAAA	957
QY	960	GAAGAACCAAGATCTCTCTCTCCCATCTAATAATTTCTCCGCCCTTTTCCCTCTCTAT	1019
Db	958	GAAGAACCAAGATCTCTCTCTCTCCCATCTAATAATTTCTCCGCCCTTTTCCCTCTCTAT	1017
QY	1020	ATAGAGGCGATCCAAAGCCAGAAAGAGGAGAGACCAAGACACGCGCATATGACAGAAACC	1079
Db	1018	ATAGAGGCGATCCAAAGCCAGAAAGAGGAGAGACCAAGAGACGCGCATATGACAGAAACC	1077

QY 1080 GAGCGACGGCCTTCCTGATCCATATCTTCGGTCGAGTTCTTGCTGATCTCTCCCTC 1139
DB 1078 GAGCGACGGCCTTCCTGATCCATATCTTCGGTCGAGTTCTTGCTGATCTCTCCCTC 1137
QY 1140 CTCACCTCTCTCTCAAGGATATGCGCCCTCGGTTGTTCTTGATTTATTTGTTCTAG 1199
DB 1138 CTCACCTCTCTCTCAAGGATATGCGCCCTCGGTTGTTCTTGATTTATTTGTTCTAG 1197
QY 1200 TTGTGATGACGGGCGTTGATGTTAGAAAAGGGATCTGTATCTGATGATCTCTGTC 1259
DB 1198 TTGTGATGACGGGCGTTGATGTTAGAAAAGGGATCTGTATCTGATGATCTCTGTC 1257
QY 1260 TTGATTTGGGATAGAGGGGTTCTGTATGTCATGTTACGGTTGCTTGAATAGAG 1319
DB 1258 TTGATTTGGGATAGAGGGGTTCTGTATGTCATGTTACGGTTGCTTGAATAGAG 1317
QY 1320 TATGTTTTCATCGTCTGAGAGCTCTATGAAATGAATGTTTACGGTACGGATCT 1379
DB 1318 TATGTTTTCATCGTCTGAGAGCTCTATGAAATGAATGTTTACGGTACGGATCT 1377
QY 1380 TCGATTTTGTAGTACCTTTTGTGAGTAAATCAGAGCAGGGTATTTGCTTG 1439
DB 1378 TCGATTTTGTGA-TACCTTTTGTGAGTAAATCAGAGCAGGGTATTTGCTTG 1436
QY 1440 TGTATTAAGATACATTTTGTGCTCTGATTTCTGTAGTATGCTTCTGATTTGAG 1499
DB 1437 TGTATTAAGATACATTTTGTGCTCTGATTTCTGTAGTATGCTTCTGATTTGAG 1496
QY 1500 AAGCTATCTTGTGTTATTCCTATTTGAACAAAATATTCATCTTGAAGAGGTCGG 1559
DB 1497 AAGCTATCTTGTGTTATTCCTATTTGAACAAAATATTCATCTTGAAGAGGTCGG 1556
QY 1560 TTGATGATGATGATGATGATTTCTTACGCTGTCGAAATTTGAGCGGCTTTTA 1619
DB 1557 TTGATGATGATGATGATGATTTCTTACGCTGTCGAAATTTGAGCGGCTTTTA 1616
QY 1620 GATACAGTATCCCATCAAGAAATCATGAAAAGATTATATCTTCAGAAACAGGGA 1679
DB 1617 GATACAGTATCCCATCAAGAAATCATGAAAAGATTATATCTTCAGAAACAGGGA 1676
QY 1680 TTCCCTGTTCTCCGATTTGCTTACCTCCAGAAATTTTTCCTCAATATCTTAAAG 1739
DB 1677 TTCCCTGTTCTCCGATTTGCTTACCTCCAGAAATTTTTCCTCAATATCTTAAAG 1736
QY 1740 TCACCTTCGTTCACTTCAATGAATGATGTTGCTAATATGCTTTATAGCGTTATC 1799
DB 1737 TCACCTTCGTTCACTTCAATGAATGATGTTGCTAATATGCTTTATAGCGTTATC 1796
QY 1800 CTAGCTGATGTTCACTTATAGGTAATACCCCTATAGTTAGTCAGAGAAAGAACTTATC 1859
DB 1797 CTAGCTGATGTTCACTTATAGGTAATACCCCTATAGTTAGTCAGAGAAAGAACTTATC 1856
QY 1860 CGATTTCTGATCTCAATTTTAAATTAATGAATGAAGTGAAGCATTAAGCATTTAT 1919
DB 1857 CGATTTCTGATCTCAATTTTAAATTAATGAATGAAGTGAAGCATTAAGCATTTAT 1916
QY 1920 TGGATTAATTTTAAATTAATAGCTTCAACCCCTCATATTTCTAGCTGAAGTCTGGCAG 1979
DB 1917 TGGATTAATTTTAAATTAATAGCTTCAACCCCTCATATTTCTAGCTGAAGTCTGGCAG 1975
QY 1980 AACTGCTCAATTTTGTGTTCAAAATTCATGATATTCATGATATTCCTCTGTAT 2039
DB 1976 AACTGCTCAATTTTGTGTTCAAAATTCATGATATTCATGATATTCCTCTGTAT 2035
QY 2040 CTACCTGTAAGATTTCTTTTGTGTTATTCCTGACTGCTGATTAACAGAAAGAAATTTA 2099
DB 2036 CTACCTGTAAGATTTCTTTTGTGTTATTCCTGACTGCTGATTAACAGAAAGAAATTTA 2095
QY 2100 TGAAGCTGTAATCGGATGATATTAATGCTGTTCTTATGATTTCTTTGTCAGT 2159
DB 2096 TGAAGCTGTAATCGGATGATATTAATGCTGTTCTTATGATTTCTTTGTCAGT 2155
QY 2160 TCTTGCTGATGCTTGCCACTTTCACAGAAAGTTTC 2195

DB 2156 TCTTGCTGATGCTTGCCACTTTCACAGCAAGTTTC 2191
RESULT 5
AAC88400
ID AAC88400 standard; DNA; 898 BP.
XX AAC88400;
AC AAC88400;
XX
DT 02-MAR-2001 (first entry)
XX
DE Rice GOS2 enhancer.
XX
KM Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;
XX herbicide resistance; se.
OS
XX Oryza sativa.
XX
PN WO20066746-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000WO-GB001559.
XX
PR 29-APR-1999; 99GB-00009971.
PR 29-APR-1999; 99GB-00009972.
PR 29-JUL-1999; 99GB-00017837.
PR 29-JUL-1999; 99GB-00017842.
PR 21-DEC-1999; 99GB-00030190.
PR 21-DEC-1999; 99GB-00030206.
PR 21-DEC-1999; 99GB-00030214.
PR 21-DEC-1999; 99GB-00030216.
XX
XX (ZENRE) ZENECA LTD.
XX
PI Hawkes TR, Warner SMJ, Andrews CJ, Bachoo S, Pickerrill AP;
XX
DR WPI; 2000-679763/66.
XX
PT Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate
XX synthase, used to produce glyphosate tolerant or resistant plants.
XX
PS Disclosure; Page 55; 85pp; English.
XX
CC The present invention relates to a glyphosate resistant rice 5-
CC enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can be
CC used to produce plant tissue and/or morphologically normal fertile whole
CC plants which are tolerant or resistant to glyphosate herbicide, and in
CC the production of a herbicidal target for the high throughput in vitro
CC screening of potential herbicides
XX
SQ Sequence 898 BP; 320 A; 166 C; 137 G; 275 T; 0 U; 0 Other:
Query Match 39.5%; Score 867.2; DB 3; Length 898;
Best Local Similarity 99.2%; Pred. No. 7.4e-184;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;
QY 1 AATCGAAAAGTTTTCGACCGTTTTCACGCTCTTAACATATATAGGAAACGTTGCT 60
DB 2 AATCGAAAAGTTTTCGACCGTTTTCACGCTCTTAACATATATAGGAAACGTTGCT 61
QY 61 AATATTAATAGACCTTATATATGCGCTGATTAAGTCTTAAGTCTTAAGTCTTAAGTCT 120
DB 62 AATATTAATAGACCTTATATATGCGCTGATTAAGTCTTAAGTCTTAAGTCTTAAGTCT 121
QY 121 CATCCACCTACTTATGTCGCAATCGGGCTAATATAAAGAGTCTCACTAGTTTGT 180
DB 122 CATCCACCTACTTATGTCGCAATCGGGCTAATATAAAGAGTCTCACTAGTTTGT 181
QY 181 TTTCTTGAATATTAAGTGGGAAATGAATCATTTGCTTGAATATTAAGTCTTCAATC 240
DB 182 TTTCTTGAATATTAAGTGGGAAATGAATCATTTGCTTGAATATTAAGTCTTCAATC 241

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QY 241 TCTGTCATGAGTAAATTAATTCGAGTAGCCATAATTCATCAAACTCTTCTGAATA 300
    |||
DB 242 TCTGTCATGAGTAAATTAATTCGAGTAGCCATAATTCATCAAACTCTTGAATA 301
QY 301 AAAAAATCTTTCTAGCTGAACATCGGTAAAGAGATTTTTTTTTTAAAAAAT 360
    |||
DB 302 AAAAAATCTTTCTAGCTGAACATCGGTAAAGAGATTTTTTTTTT---AAAAAAT 358
QY 361 AGAATGAGATATTCGAGCGTATCGGCAAGATTTAAACATATATATATATATAT 420
    |||
DB 369 AGAATGAGATATTCGAGCGTATCGGCAAGATTTAAACATATATATATATATAT 418
QY 421 AGTTTGTCATTCGTTATATCGCACGCTATTAAGAATGCTTACTCCATCTCAATTT 480
    |||
DB 419 AGTTTGTCATTCGTTATATCCAGCTCATTAAGAATGCTTACTCCATCTCAATTTT 478
QY 481 TATTTAGTAAATTAAGACATTAATTTATTTATTTATTTATTTTTCGATTAATTC 540
    |||
DB 479 TATTTAGTAAATTAAGACATTAATTTATTTATTTATTTATTTTTCGATTAATTC 538
QY 541 AAGGTACTTAGGACACACACTTTGTGCTCATGTGATGATGATGACCTCCGTC-ATACA 599
    |||
DB 539 AAGGTACTTAGGACACACACTTTGTGCTCATGTGATGATGATGACCTCCGTCATACA 598
QY 600 CGTTCAACTAGGACACACATCTCCATATCTCGCTATTTATATACATTTAGTAGCAAT 659
    |||
DB 599 CGTTCAACTAGGACACACATCTCCATATCTCGCTATTTATATACATTTAGTAGCAAT 658
QY 660 ATCTGAATTCAGCACTTACCATCCACGACCACTTTTAATATATCTTAATACAAAA 719
    |||
DB 659 ATCTGAATTCAGCACTTACCATCCACGACCACTTTTAATATATCTTAATACAAAA 718
QY 720 AATTAATTTACGAATAGCATGAAAAAGTATGAACGATTTTAGTTTTCACATACA 779
    |||
DB 719 AATTAATTTACGAATAGCATGAAAAAGTATGAACGATTTTAGTTTTCACATACA 778
QY 780 AAAAAAAGAAATTTTGTGCTGCGCGACGCCCAATCTCCATATTTGGGACACAGGCA 839
    |||
DB 779 AAAAAAAGAAATTTTGTGCTGCGCGACGCCCAATCTCCATATTTGGGACACAGGCA 838
QY 840 ACAACAGAGTGGCTGCCACAGAACCAACCAAAAGATGATCTAACGAGGACAGC 899
    |||
DB 839 ACAACAGAGTGGCTGCCACAGAACCAACCAAAAGATGATCTAACGAGGACAGC 898

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RESULT 7
AAC87195
ID AAC87195 standard; DNA; 898 BP.

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XX AAC87195;
XX
DT 09-MAR-2001 (first entry)
XX
DE Rice GOS2 promoter enhancer element, SEQ ID NO:50.
XX
KW Rice EPSPS; 5-enolpyruvylshikimate phosphatase;
    glyophosphate resistance; herbicide resistance; transgenic plant;
    expression construct; enhancer element; ds.
XX
OS Oryza sativa.
XX
PN MO200066748-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000WO-GB001573.
XX
PR 29-APR-1999; 99GB-00009968.
XX
PR 29-JUL-1999; 99GB-00017834.
XX
PR 29-JUL-1999; 99GB-00017839.
XX
PR 29-JUL-1999; 99GB-00017840.
XX
PR 29-JUL-1999; 99GB-00017846.

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PR 29-JUL-1999; 99GB-00017847.
PR 21-DEC-1999; 99GB-00030200.
PR 21-DEC-1999; 99GB-00030204.
PR 21-DEC-1999; 99GB-00030207.
PR 21-DEC-1999; 99GB-00030209.
PR 21-DEC-1999; 99GB-00030213.
XX
PA (ZENEC ) ZENEC LTD.
XX
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;
DR WPI; 2000-687544/67.
XX
PT Novel polynucleotide encoding 5-enolpyruvylshikimate phosphatase,
PT having resistance or tolerance to glyphosate herbicide.
XX
PS Claim 18; Page 56; 87pp; English.
XX
CC The invention relates to rice 5-enolpyruvylshikimate phosphatase
CC (EPSPS) genomic DNA (AAC87188). The invention also relates to an
CC expression cassette comprising, in the 5'-3' direction, one or more
CC transcriptional enhancer elements selected from AAC87190-C87196), the
CC rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast
CC transit peptide, genomic DNA encoding a EPSPS protein modified such that
CC it is resistant to glyphosate (AAC87189), and a transcriptional
CC terminator. The glyphosate resistant EPSPS contains a region (AAB29793)
CC containing two amino acid substitutions relative to the corresponding
CC wild-type region (AAB29792). The invention also encompasses plant genomic
CC EPSPS sequences identified via screening with a rice EPSPS intronic
CC sequence; vectors and host plant cells comprising a nucleic acid sequence
CC of the invention; transgenic plants (and tissues and seeds thereof)
CC comprising a nucleic acid sequence of the invention, optionally further
CC transformed with a DNA encoding an insect, fungal, viral, bacterial,
CC nematode, stress or herbicide resistance protein; and methods of
CC producing the transgenic plants of the invention. The nucleic acids and
CC constructs of the invention are used to produce a wide variety of
CC morphologically normal, glyphosate resistant plants. The glyphosate
CC resistant plants produced are particularly maize, soybean, cotton,
CC sugarbeet and canola, but also other field crops, fruits and vegetables,
CC turf and forage grasses and nut-producing plants. The plants are
CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,
CC stress, desiccation and/or other herbicides. They can be used in the
CC production of a herbicidal target for the high throughput in vitro
CC screening of potential herbicides. The present sequence represents an
CC enhancer element which may be used in the rice EPSPS expression cassette
CC of the invention
XX
SQ Sequence 898 BP; 166 C; 137 G; 275 T; 0 U; 0 Other;

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Query Match 39.5%; Score 867.2; DB 3; Length 898;
Best Local Similarity 99.2%; Pred. No. 7,4e-184;
Matches 893; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

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QY 1 AATCCGAAAAGTTTCTGACCGCTTTTCAGTCTTCTTAACATATATAGGAACTGTCT 60
    |||
DB 2 AATCCGAAAAGTTTCTGACCGCTTTTCAGTCTTCTTAACATATATAGGAACTGTCT 61
QY 61 AATATTAATGAGACCTTATATATATGAGCGCTGTAAGAACTATATAGAAAACT 120
    |||
DB 62 AATATTAATGAGACCTTATATATATGAGCGCTGTAAGAACTATATAGAAAACT 121
QY 121 CATCACCCTACTTATAGTGGCAATCGGGCTAATATAAAAAGAGTGGCTACCTAGTTTCT 180
    |||
DB 122 CATCACCCTACTTATAGTGGCAATCGGGCTAATATAAAAAGAGTGGCTACCTAGTTTCT 181
QY 181 TTTCTTATGTAATTAAGTGGGAAAAATGAATCATTTATGCTTAAGATATAGTTTCATC 240
    |||
DB 182 TTTCTTATGTAATTAAGTGGGAAAAATGAATCATTTATGCTTAAGATATAGTTTCATC 241
QY 241 TCTGTCATGAGTAAATTAATTCGAGTAGCCATAATTCATCAAACTCTTCTGAATA 300
    |||
DB 242 TCTGTCATGAGTAAATTAATTCGAGTAGCCATAATTCATCAAACTCTTCTGAATA 301

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Db      1201 TCTTAAAGTAAGAAAAAAGCCGCTTCTTAATGTAATTCATTTCTTAAACCAAGC 1142
QY      199  GGGAAATGAAATCATTAATGTTAGATATACGTTCACTCTGTGATGAATTAAT 258
      1141 GGGAAATGAAATGTTAGTACCTAGAAAGGACGTCACTGATTAATTAAT 1082
QY      259  TATTCAGGTAGGCGATTAATGTCATCAAACTCTTCTTG-----AATTAATAATCTTTC 312
      1081 TCTTGAAGGTGCGCATGATTAATATGCAATCATCTAGCGTAACAAAGAAATGATGTTTC 1022
Db      313  TAGCTGAATCAATGGGTAAGAGATATTTTAAAAAAAATAGAAATGAAT 372
QY      1021 TAGCCAAATCAATGATCAAGATGAGGGAACCTTTTAAAAAATGAATAGG 962
QY      373  TTCTGAACGATCGGCAAAAGATTAAACATATATATATATATATAG 422
Db      961  AAGAAACATATATGAAATTAATGTCCTTGTATGAAATATGAAATTTTG 912

RESULT 15
ABD33574
ID      ABD33574 standard; DNA; 101954 BP.
XX      ABD33574;
AC      ABD33574;
XX      18-NOV-2004 (first entry)
DT
XX      Human cancer-associated (CA) gene HD07-115.
XX      Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
XX      de; cancer; cytostatic.
XX      Homo sapiens.
OS      WO2004058146-A2.
XX      15-JUL-2004.
PD      15-DEC-2003; 2003WO-US040081.
XX      17-DEC-2002; 2002US-00322281.
PR      (SAGR-) SAGRES DISCOVERY INC.
XX      (SAGR-) SAGRES DISCOVERY INC.
XX      Morris DM, Malandro MS;
PI      MPI; 2004-499109/47.
XX      Novel human cancer associated protein encoded within open reading frame
XX      of cancer associated gene, useful as targets for diagnosing cancer.
PT      Claim 16; SEQ ID NO 782; 182bp; English.
PS
XX      The invention relates to cancer-associated proteins (CAP) and the cancer-
XX      associated (CA) nucleic acids encoding them. The invention also relates
XX      to a method for treating cancers involving administering to a patient an
XX      inhibitor of CAP, and a method of screening for anticancer activity in a
XX      potential drug involving providing a cell that expresses a CA gene,
XX      contacting a tissue sample derived from a cancer cell with an anticancer
XX      drug candidate and monitoring the effect of the anticancer drug candidate
XX      on expression of the CA gene. The CAP proteins are useful for detecting
XX      cancer associated with expression of a CAP protein in a test cell sample
XX      and for screening for a bioactive agent capable of modulating the
XX      activity of a CAP protein. The CA nucleic acids are useful for diagnosing
XX      cancer, involving determining the expression of a CA nucleic acid in a
XX      tissue. This sequence represents a human CA gene of the invention. Note:
XX      The sequence data for this patent did not form part of the printed
XX      specification, but was obtained in electronic format directly from WIPO
XX      at ftp.wipo.int/pub/published_pct_sequences
XX      Sequence 101954 BP; 29500 A; 18891 C; 19534 G; 32684 T; 0 U; 1345 Other;
SQ
Query Match      2.5%; Score 55.6; DB 13; Length 101954;
```

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Best Local Similarity 50.6%; Pred. No. 0.1;
Matches 162; Conservative 0; Mismatches 154; Indels 4; Gaps 1;
QY      225  AATATACGTTCAATCTCTGTCATGAAGTTAATTATTCGAGGTAGCCATTAATGTCATC 284
      74856 AACATGAGTGAACCGCTCTCTCAAAAAATATATATATGTGTTGTATGTATATATATAA 74915
Db      285  AAACCTTCTGTAATAAAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTT 344
QY      74916 AATATATATTAATATTAATTAATATATTAATTAATTAATTAATTAATTAATTAAT 74975
Db      345  TTTTAAAAAAATAGATGAATATTCGAACGTATCGGCAAGATTAAACATAT 404
QY      74976 TAATATATTAATAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 75035
QY      405  AATATATATTAATTTTATAGTTGTGCAATGCTATATATCGACGTCATTAAGACATGCTTT 464
Db      75036 AATATATATGATATATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 75095
QY      465  ACTGCATCTCAAT---TTTATTTAGTAAATTAAGACAAATGACTTATTTTATATTT 520
Db      75096 TCTTTAAGGGAAGCTACTTTTCTTTCCTGCACAAAATAGTAGTACTGTTTATATATAT 75155
QY      521  ATCTTTTTCGATTAAGATGC 540
Db      75156 GTTTTATATCTTTTAGTGC 75175
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Job time : 1231 secs

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OM nucleic - nucleic search, using bw model

Run on: April 21, 2006, 08:53:59 ; Search time 2181 Seconds
(without alignments)
4072.581 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195
Sequence: 1 aatccgaagaagttctgcac.....cacttcaccagcaagttc 2195

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 9288580 seqs, 2023302648 residues

Total number of hits satisfying chosen parameters: 18577160

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications_NA_New:*
1: /SIDS5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	100.0	2195	9	US-10-541-315-1
2	1166	53.1	1176	14	US-11-128-549-2
3	1099.2	50.1	1112	14	US-11-128-549-1
4	987.8	45.0	999	14	US-11-128-549-5
5	51.8	2.5	171486	14	US-11-121-086-105
6	49.6	2.3	672	6	US-09-925-065A-673832
7	49.2	2.2	672	6	US-11-096-568A-21310
8	49.2	2.2	906	11	US-10-893-483-184
9	49	2.2	1739	9	US-10-893-483-186
10	49	2.2	36259	9	US-10-893-483-186
11	49	2.2	39794	14	US-11-098-686-8737
12	48.4	2.2	6152	14	US-11-196-400-1
13	48.2	2.2	624	6	US-09-925-065A-946580
14	48.2	2.2	995	10	US-10-301-480-546623
15	48.2	2.2	995	10	US-10-301-480-1160032
16	48.2	2.2	997	10	US-10-301-480-546624
17	48.2	2.2	997	10	US-10-301-480-1160033
18	47.6	2.2	591	6	US-09-925-065A-387578

C	19	47.6	2.2	591	6	US-09-925-065A-387580	Sequence 387580,
	20	47.6	2.2	595	10	US-10-301-480-456079	Sequence 456079,
	21	47.6	2.2	595	10	US-10-301-480-456081	Sequence 456081,
	22	47.6	2.2	595	10	US-10-301-480-1069488	Sequence 1069488,
	23	47.6	2.2	595	10	US-10-301-480-1069490	Sequence 1069490,
	24	47.6	2.2	807	10	US-10-301-480-586745	Sequence 586745,
	25	47.6	2.2	590	9	US-10-301-480-1200154	Sequence 1200154,
	26	47.4	2.2	590	9	US-10-301-480-59750	Sequence 59750, A
	27	47.4	2.2	590	9	US-10-301-480-59751	Sequence 59751, A
	28	47.4	2.2	590	9	US-10-301-480-59753	Sequence 59753, A
	29	47.4	2.2	590	10	US-10-301-480-673159	Sequence 673159,
	30	47.4	2.2	590	10	US-10-301-480-673160	Sequence 673160,
	31	47.4	2.2	590	10	US-10-301-480-673162	Sequence 673162,
	32	47.4	2.2	670	10	US-10-301-480-561044	Sequence 561044,
	33	47.4	2.2	670	10	US-10-301-480-1174453	Sequence 1174453,
	34	47.2	2.2	591	6	US-09-925-065A-387579	Sequence 387579,
	35	47.2	2.2	595	10	US-10-301-480-456080	Sequence 456080,
	36	47.2	2.2	595	10	US-10-301-480-1069489	Sequence 1069489,
	37	47	2.1	590	9	US-10-301-480-59752	Sequence 59752, A
	38	47	2.1	590	10	US-10-301-480-673161	Sequence 673161,
	39	46.8	2.1	105550	8	US-10-995-561-13235	Sequence 13235, A
	40	46.8	2.1	194553	14	US-11-098-686-8738	Sequence 8738, AP
	41	46.6	2.1	26772	8	US-10-995-561-13313	Sequence 13313, A
	42	46.6	2.1	54946	8	US-10-995-561-13479	Sequence 13479, A
	43	46.4	2.1	585	6	US-09-925-065A-336359	Sequence 336359,
	44	46.4	2.1	585	6	US-09-925-065A-336360	Sequence 336360,
	45	46.4	2.1	602	10	US-10-301-480-409672	Sequence 409672,

ALIGNMENTS

RESULT 1
US-10-541-315-1
Sequence 1, Application US/10541315
Publication No. US20060053507A1
GENERAL INFORMATION:
APPLICANT: CropDesign N.V.
TITLE OF INVENTION: Regulatory sequence
FILE REFERENCE: CD-072-PCT
CURRENT APPLICATION NUMBER: US/10/541, 315
PRIOR FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: EP 03075207.5
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2195
TYPE: DNA
ORGANISM: Oryza sativa
US-10-541-315-1

Query Match	100.0%	Score 2195	DB: 9	Length 2195
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2195	Conservative	0	Mismatches	0
QY	1		1	
DB	1		1	
QY	61		61	
DB	61		61	
QY	121		121	
DB	121		121	
QY	181		181	
DB	181		181	
QY	241		241	
DB	241		241	

Db	241	TCGTGATGAACTTAAATATTTGAGAGTACCATATTTGTATCAAACTCTTGAAATA	300
Qy	301	AAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTAAAAAAAAT	360
Db	301	AAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTAAAAAAAAT	360
Qy	361	AGAAAGAAAGATATTTCTGAAACGTATGGGCAAAATTTAAACATATAATATATATTTAT	420
Db	361	AGAAAGAAAGATATTTCTGAAACGTATGGGCAAAATTTAAACATATAATATATATTTAT	420
Qy	421	AGTTGTGCATTCGTTATATCGCAGCTCATTAAGACATGTCTTACCTCAATTTT	480
Db	421	AGTTGTGCATTCGTTATATCGCAGCTCATTAAGACATGTCTTACCTCAATTTT	480
Qy	481	TATTTAGTAATTTAAAGACAATTGACTATTTTTATTTATCTTTTTCGATAGATGC	540
Db	481	TATTTAGTAATTTAAAGACAATTGACTATTTTTATTTATCTTTTTCGATAGATGC	540
Qy	541	AAGTAATCTTAAGCACACACTTTGTGCTCATGTGCAATGTGTAGTGCACCTCTCATAC	600
Db	541	AAGTAATCTTAAGCACACACTTTGTGCTCATGTGCAATGTGTAGTGCACCTCTCATAC	600
Qy	601	GTTCAACTAGGACACATCTCCAAATATCACTGGCTATTTAATACATTTAGGTAGCAATA	660
Db	601	GTTCAACTAGGACACATCTCCAAATATCACTGGCTATTTAATACATTTAGGTAGCAATA	660
Qy	661	TCTGAATTCAGCACTTCACATCACAGACCAACCTTTTAAATATCTAAATACAAAAA	720
Db	661	TCTGAATTCAGCACTTCACATCACAGACCAACCTTTTAAATATCTAAATACAAAAA	720
Qy	721	ATAATTTTACAGATATGCAATGAAAAAGTATGAAACGATATTTAGTTTTTCACTATACA	780
Db	721	ATAATTTTACAGATATGCAATGAAAAAGTATGAAACGATATTTAGTTTTTCACTATACA	780
Qy	781	AAAAAAAAGAAATTTTGCTCGTGGCGGAGCGGCATCTCCCATTTTGGGACACACGGCA	840
Db	781	AAAAAAAAGAAATTTTGCTCGTGGCGGAGCGGCATCTCCCATTTTGGGACACACGGCA	840
Qy	841	CAACAGAGTGGCTGCCCCACAGAACCAACCAAAAAAGATGATCTAACGAGNACAGCA	900
Db	841	CAACAGAGTGGCTGCCCCACAGAACCAACCAAAAAAGATGATCTAACGAGNACAGCA	900
Qy	901	AGTCCGCAACAACTTTTAAACAGCAGGCTTTGCGGCAGAGAGAGAGAGAGGCAAG	960
Db	901	AGTCCGCAACAACTTTTAAACAGCAGGCTTTGCGGCAGAGAGAGAGAGAGGCAAG	960
Qy	961	AAAAACAAGACCTCTCTCCATCTTAATCTCTCCGCCCTTTTCCCTCTCTATA	1020
Db	961	AAAAACAAGACCTCTCTCCATCTTAATCTCTCCGCCCTTTTCCCTCTCTATA	1020
Qy	1021	TAGAGAGCATCCAAACCAAGAGAGAGAGACCAAGACACGCGCATAGCAGAAAGCG	1080
Db	1021	TAGAGAGCATCCAAACCAAGAGAGAGAGACCAAGACACGCGCATAGCAGAAAGCG	1080
Qy	1081	AGCGACGCGCTTCTTGATTCATATCTTCCGATCGATGTTCTTGATCTCTTCCCTCC	1140
Db	1081	AGCGACGCGCTTCTTGATTCATATCTTCCGATCGATGTTCTTGATCTCTTCCCTCC	1140
Qy	1141	TCCACCTCTCTCTCAACAGGATATGAGCCCTTCGGTTGTTCTTGAAATTAATGTTCTAGT	1200
Db	1141	TCCACCTCTCTCTCAACAGGATATGAGCCCTTCGGTTGTTCTTGAAATTAATGTTCTAGT	1200
Qy	1201	TGTGTAGTACGGGCGCTTGATGTTAGAAAGGGGACTGTATCTGATGATCTCTGTTCT	1260
Db	1201	TGTGTAGTACGGGCGCTTGATGTTAGAAAGGGGACTGTATCTGATGATCTCTGTTCT	1260
Qy	1261	TGGATTTGGATATGAGGGGTTCTTATGTGCAATGTATCGGTTGCGTTGATTAATGATG	1320
Db	1261	TGGATTTGGATATGAGGGGTTCTTATGTGCAATGTATCGGTTGCGTTGATTAATGATG	1320
Qy	1321	ATGTTTTCAATCGTCTGAGAGCTCTATGCAATGAAATGATTTAGGATACGAATCTT	1380
Db	1321	ATGTTTTCAATCGTCTGAGAGCTCTATGCAATGAAATGATTTAGGATACGAATCTT	1380

Db	1321	ATGCTTTTCAATCGCTGAGAGAGCTCATGTGAAATGAAATGGAATGTTAGGGTATCGGAATCTT	1380
Qy	1381	GGGATTTTGGAGAGACCTTTTGGTTGGAGGTAAATCAAGACACGGGATTTTGGCTGGT	1440
Db	1381	GGGATTTTGGAGACCTTTTGGTTGGAGGTAAATCAAGACACGGGATTTTGGCTGGT	1440
Qy	1441	GTAATTAAGAATACATTTGGTTGGTCCCTCGAATTCGTAGTAGATGCTTCGATTTTGACGA	1500
Db	1441	GTAATTAAGAATACATTTGGTTGGTCCCTCGAATTCGTAGTAGATGCTTCGATTTTGACGA	1500
Qy	1501	AGCTATCCCTTGGTTTATTTCCCTATTTGAACAAAAATAATCCACTTTGAAAGACGGTCCCGT	1560
Db	1501	AGCTATCCCTTGGTTTATTTCCCTATTTGAACAAAAATAATCCACTTTGAAAGACGGTCCCGT	1560
Qy	1561	TGATGAGATTTGAATGATTTGATTCCTTAAGCCCTGTCACAAATTTTGGCAGCTGGCTGTTAG	1620
Db	1561	TGATGAGATTTGAATGATTTGATTCCTTAAGCCCTGTCACAAATTTTGGCAGCTGGCTGTTAG	1620
Qy	1621	ATACAGTAGTCCCATCAGCAAAATTCATGAAAAACAGTTATATACCTCAGGAACAGGGGAT	1680
Db	1621	ATACAGTAGTCCCATCAGCAAAATTCATGAAAAACAGTTATATACCTCAGGAACAGGGGAT	1680
Qy	1681	TCCCTGTTCTCTCCGATTTGCTTTAGTCCAGAAATTTTTTTTCCCAATATCTTAAAAAGT	1740
Db	1681	TCCCTGTTCTCTCCGATTTGCTTTAGTCCAGAAATTTTTTTTCCCAATATCTTAAAAAGT	1740
Qy	1741	CACTTTCTGGTTCAGTTCAATGAAATGATTCGTAACAATAAGTTTATATAGCTTATATCC	1800
Db	1741	CACTTTCTGGTTCAGTTCAATGAAATGATTCGTAACAATAAGTTTATATAGCTTATATCC	1800
Qy	1801	TAGCTGATGTTCACTTATATAGGTAAATCCCTATAGTTTAGTCAGAGAAAGAACTTATCC	1860
Db	1801	TAGCTGATGTTCACTTATATAGGTAAATCCCTATAGTTTAGTCAGAGAAAGAACTTATCC	1860
Qy	1861	GATTTCTGATCTCCATTTTAAATTATATGAAATGAACGTAGACATTAAGCAATATTCATTT	1920
Db	1861	GATTTCTGATCTCCATTTTAAATTATATGAAATGAACGTAGACATTAAGCAATATTCATTT	1920
Qy	1921	GGATTTATTTTTTATTTATAGCTTCAACCCCTTCATTTATTCGAGCTGAAAGTCTGGCATGA	1980
Db	1921	GGATTTATTTTTTATTTATAGCTTCAACCCCTTCATTTATTCGAGCTGAAAGTCTGGCATGA	1980
Qy	1981	ACGTGCTCAATTTTGGTTTCAAAATTCACATTCGATATTCATGCAATATCCTCTGTATTC	2040
Db	1981	ACGTGCTCAATTTTGGTTTCAAAATTCACATTCGATATTCATGCAATATCCTCTGTATTC	2040
Qy	2041	TACCTGTAGAAAGTTCTTTTGGTTATTCCTGTGACCTGATTAAGAAAGAAATTTAT	2100
Db	2041	TACCTGTAGAAAGTTCTTTTGGTTATTCCTGTGACCTGATTAAGAAAGAAATTTAT	2100
Qy	2101	GAACTGTAAATCGGAGATAGTTATCTCTGTTCTTATGATTCATTTCTTTTGGCAGTT	2160
Db	2101	GAACTGTAAATCGGAGATAGTTATCTCTGTTCTTATGATTCATTTCTTTTGGCAGTT	2160
Qy	2161	CTTGCTGATGTTGGCACTTCAACCAAGAAAGTTC	2195
Db	2161	CTTGCTGATGTTGGCACTTCAACCAAGAAAGTTC	2195
RESULT 2			
US-11-128-549-2			
; Sequence 2, Application US/11128549			
; Publication No. US20050262597A1			
; GENERAL INFORMATION:			
; APPLICANT: Broekaert, Willem			
; APPLICANT: De Wilde, Chris			
; APPLICANT: Hatzfeld, Yves			
; APPLICANT: Zhou, Zhongyi			
; TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION			
; FILE REFERENCE: 1187-40			
; CURRENT APPLICATION NUMBER: US/11/128, 549			
; CURRENT FILING DATE: 2005-05-13			
; PRIOR APPLICATION NUMBER: US 60/572, 141			


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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 673832
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-673832

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Query Match      2.3%; Score 49.6; DB 6; Length 672;
Best Local Similarity 47.2%; Pred. No. 4.5;
Matches 185; Conservative 1; Mismatches 200; Indels 6; Gaps 1;

Qy 155 AAAAAAGTCGCTACCTAGTTCCGTTCCCTAGTAATTAAGTGGAAATGAATCAT 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 418 ATAAATAAATAATACCTTTGTAATAATAATAATAATAATAATAATAATAATA 359

Qy 215 TATTCCTAGAAATATACGTTCAATCTGTCATGAGTAAATATTCAGAGTACCAT 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 358 TATTCCTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 299

Qy 275 AATGTCATCAAACTCTCTCTGTAATAAAAAATCTTTAGCTGAACCTCAATGGGTAAG 334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 AATATATATAATA-----TATTAATGAATAATACATCTTTTAAATAATATATATATAT 245

Qy 335 AAGAGATATTTTTTTTAAAAAAAATAGAAATGAAGATATTCGAACGTACGCAAAAGAT 394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 ACATAAATATATATATTTTCCATATAATAATAATAATAATAATAATAATAATA 185

Qy 395 TTTAAACATATATATATATATATATATATATATATATATATATATATATATAT 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TTTATGATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 125

Qy 455 GACATGCTTACTCCATCTCAATTTTATATTAAGTAATAAGCAATGACTTATTTTAA 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 TATTTATATATATATATATATATATATATATATATATATATATATATATATAT 65

Qy 515 TTTATTTATCTTTTTCGATTAGATGCAAGTA 546
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 64 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 33

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RESULT 8
US-11-096-568A-21310
; Sequence 21310, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21310
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(906)
; OTHER INFORMATION: Ceres Seq. ID no. 12402928
US-11-096-568A-21310

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```

Query Match      2.2%; Score 49.2; DB 11; Length 906;
Best Local Similarity 80.4%; Pred. No. 5.9;
Matches 82; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

Qy 968 AGCATCTCTCCCTCCCATCTATAATTCCTCCCTCTCTCTATATAGAGG 1027
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 ACCGTCCTCTCTCTCCCTCTATAATTC--CTCTCTTTCTCTCTCATATATAGGGC 138

Qy 1028 CATCCAGCCAAAGAGAGG--AGAGCACCAGACGACCGAC 1068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 CATCAGATCCAAAGAGAGAGGAGACCAAGACCTTCGGC 180

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RESULT 9
US-10-893-483-184
; Sequence 184, Application US/10893483
; Publication No. US20060026696A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Plazzer, Josef
; APPLICANT: Schooten, Wim van
; TITLE OF INVENTION: Humanized Immunoglobulin Loc1
; FILE REFERENCE: 39691-0007A
; CURRENT APPLICATION NUMBER: US/10/893,483
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: 60/487,733
; PRIOR FILING DATE: 2003-07-15
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 1739
; TYPE: DNA
; ORGANISM: Gallus domesticus
US-10-893-483-184

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```

Query Match      2.2%; Score 49; DB 9; Length 1739;
Best Local Similarity 52.2%; Pred. No. 8.1;
Matches 109; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 326 TGGGTAAAGAGATATTTTTTTTAAAAAAAATAGATGAGATATTCGAACGTATC 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 507 TGTCAAAAAAGAGAGGTATTCCTGTAAGAGAGAGATATTTGTCATTTTTT 566

Qy 386 GGCAGAGATTTAAACATATATATATATATATATATATATATATATATATATAT 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 567 CGGAATATATATATATATATATATATATATATATATATATATATATATATAT 626

Qy 446 GTCATTAAGAGATCTCTACCTCCATCTCAATTTTATATTAAGTAATAAGCATGAC 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 627 TATATATATATATATATATATATATATATATATATATATATATATATATAT 686

Qy 506 TTAATTTATATATATATATATATATATATATATATATATATATATATATAT 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 687 ATATTTCTCCCTCTTTCTTTATATATATTT 715

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RESULT 10
US-10-893-483-186
; Sequence 186, Application US/10893483
; Publication No. US20060026696A1
; GENERAL INFORMATION:
; APPLICANT: Buelow, Roland
; APPLICANT: Plazzer, Josef
; APPLICANT: Schooten, Wim van
; TITLE OF INVENTION: Humanized Immunoglobulin Loc1
; FILE REFERENCE: 39691-0007A
; CURRENT APPLICATION NUMBER: US/10/893,483

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:
: CURRENT FILING DATE: 2004-07-15
: PRIOR APPLICATION NUMBER: 60/487,733
: PRIOR FILING DATE: 2003-07-15
:
: NUMBER OF SEQ ID NOS: 460
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 186
: LENGTH: 36259
: TYPE: DNA
: ORGANISM: Gallus domesticus
: US-10-893-483-186

```

Query Match	2.2%	Score 49;	DB 9;	Length 36259;
Best Local Similarity	52.2%;	Pred. No. 23;		
Matches 109;	Conservative	0;	Mismatches 100;	Indels 0;
			Gaps	0;

[illegible]

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RESULT 11
US-11-098-686-8737/c
; Sequence 8737, Application US/11098686
; Publication No. US2006002469A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/3118
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8737
; LENGTH: 39794
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-8737

```

Query March	2.2% Score 49; DB 14; Length 39794;
Best Local Similarity	47.5%; Prod. No. 24;
Matches 145; Conservative	0; Mismatches 160; Indels 0; Gaps 0;
QY .	
191 AATTAAGTGGAAAATGAATTCATTATGCTTGGAATATACGTCACATCTCGTCATGA	250
Db 27606 AATTAATATGTAATAAATGTATATCTTAATATGAAAAAACAATAATGCATTAAGATATTAAT	27547
QY 251 AGTTAAATTTATTCGAGTAGCCATAATGTGCATCAAACTCTTCTGGAATAAAAAATCTT	310
Db 27546 TAAATATATATATTTTTCATTCACATAAATTAATATGATGATATATTTAAATTTGATTTATC	27487
QY 311 TCTAGCTGAATCAATGCTTAAGAGAGATTTTTTTTAAAAAAAATAGATGAAGA	370
Db 27486 CATACATAGTACAGTAAGAAGTATATATATTTAAAGTGAATATTCACGTAGTTATCA	27422
QY 371 TATTTGAAAGTATCGGCAAAAGATTAAACATATTAATATATATTTATAGTTTGCA	430

[illegible]

RESULT 12
US-11-196-400-1/c
; Sequence 1, Application US/11196400
; Publication No. US20050287166A1

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1  APPLICANT: DRUIHE, PIERRE
2  APPLICANT: DAUBERSIES, PIERRE
3  TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
4  FILE REFERENCE: 200773USODIV
5  CURRENT APPLICATION NUMBER: US/11/196,400
6  CURRENT FILING DATE: 2005-08-04
7  PRIOR APPLICATION NUMBER: US/09/742,086
8  PRIOR FILING DATE: 2000-12-22
9  PRIOR APPLICATION NUMBER: US 08/973,482
10 PRIOR FILING DATE: 1998-02-06
11 PRIOR APPLICATION NUMBER: PCT/FR96/00894
12 PRIOR FILING DATE: 1996-06-12
13 PRIOR APPLICATION NUMBER: FR 95/07007
14 PRIOR FILING DATE: 1995-06-13
15 NUMBER OF SEQ ID NOS: 29
16 SOFTWARE: PatentIn version 3.3
17 SEQ ID NO 1
18 LENGTH: 6152
19 TYPE: DNA
20 ORGANISM: P. falciparum
21 OS-11-196-400-1

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Query Match      2.2%; Score 48.4; DB 14; Length 6152;
Best Local Similarity 52.5%; Pred. No. 16;
Matches 106; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

Qy      346 TTTTAAATAAATAGATGAATGATATTCTGACGTATCGGCACAAGATTTAAACATATA 405
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5637 TTTTATATTTAAAATTAATAATATTCGAAAAATATAATATATATATGAAAAATATAATATTTAA 5778

Qy      406 ATTATATAATTTTATAGTTTGTCATTGGTTAATTCGACGTCATTAGAAGCATGCTTTA 465
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5777 TATATATAATTTTAAAAATTTTAAAAATTTTGTA AAAAGATCATAATATATATATATAT 5718

Qy      466 CTCCATCTCAATTTTATTTTAGTAATTAAGAACAATTGACTTATTTTATTTATTACTT 525
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5717 ATGATATATATTTATTTTATTTATATATATTTACATAATATATACATTTTATATATTTT 5658

Qy      526 TTTTCGATTGATGACGAAGTAC 547
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      5657 TTATCGATTAAATTTTATTTGTTCC 5636

RESULT 13
US-09-925-065A-946580/c
Sequence 946580, Application US//09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Mang, David G.
TITLE OR INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925_065A
CURRENT FILING DATE: 2001-08-08
PRIORITY APPLICATION NUMBER: US 60/254,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147

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/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 946580
/ LENGTH: 624
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-946580
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Query Match
Best Local Similarity 55.7%; Score 48.2; DB 10; Length 624;
Matches 113; Conservative 0; Mismatches 88; Indels 2; Gaps 1;
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Qy 365 TGAAGATATTCGAAAGTATCGGCAAGATTAAACATATATATATATATATAGTT 424
Db 201 TGACTTATTAATTAACCTTAGCTTAACACAAACATATATAGCTATACAAAACC 142
Qy 425 TGTGCAATTCGTTATATCGACGTCATTAAGACATGCTTACTCCATCTCAATTTTATT 484
Db 141 TTTCTCTTTTATATATCCCTATCTCTAAGCTCTTTCTATTTAAATTAATATTT--TT 84
Qy 485 TAGTATTTAAAGCAATTCATTTATTTATTTATTTATTTTTCGATTAGTCAGAG 544
Db 83 AATTATATATTTTAAATCACTTTTATTTTATTTTAACTTTTGTATTAATAACTAAGA 24
Qy 545 TACTTAGCACACACTTTGTGCT 567
Db 23 TACACACACACACACTTCACT 1
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RESULT 14
US-10-301-480-546623/c
/ Sequence 546623, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 546623
/ LENGTH: 995
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-546623
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Query Match
Best Local Similarity 55.7%; Score 48.2; DB 10; Length 995;
Matches 113; Conservative 0; Mismatches 88; Indels 2; Gaps 1;
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Db 854 TGACTTATTAATTAACCTTAGCTTAACACAAACATATATAGCTATACAAAACC 795
Qy 425 TGTGCAATTCGTTATATCGACGTCATTAAGACATGCTTACTCCATCTCAATTTTATT 484
Db 794 TTTCTCTTTTATATATCCCTATCTCTAAGCTCTTTCTATTTTAAATTAATATTT--TT 737
Qy 485 TAGTATTTAAAGCAATTCATTTATTTATTTATTTTATTTTTCGATTAGTCAGAG 544
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Db 736 AATTATATATTTTAAATCACTTTTATTTTACTTTTAAACTTTTGTGATAAAACTAAGA 677
Qy 545 TACTTAGCACACACTTTGTGCT 567
Db 676 TACACACACACACACTTCACT 654
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US-10-301-480-1160032/c
/ Sequence 1160032, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
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/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1160032
/ LENGTH: 995
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-1160032
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Query Match
Best Local Similarity 55.7%; Score 48.2; DB 10; Length 995;
Matches 113; Conservative 0; Mismatches 88; Indels 2; Gaps 1;
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Qy 365 TGAAGATATTCGAAAGTATCGGCAAGATTAAACATATATATATATATATAGTT 424
Db 854 TGACTTATTAATTAACCTTAGCTTAACACAAACATATATAGCTATACAAAACC 795
Qy 425 TGTGCAATTCGTTATATCGACGTCATTAAGACATGCTTACTCCATCTCAATTTTATT 484
Db 794 TTTCTCTTTTATATATCCCTATCTCTAAGCTCTTTCTATTTTAAATTAATATTT--TT 737
Qy 485 TAGTATTTAAAGCAATTCATTTATTTATTTATTTTATTTTTCGATTAGTCAGAG 544
Db 736 AATTATATATTTTAAATCACTTTTATTTTATTTTAACTTTTGTATTAATAACTAAGA 677
Qy 545 TACTTAGCACACACTTTGTGCT 567
Db 676 TACACACACACACACTTCACT 654
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Job time : 2184 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 09:00:48 ; Search time 1135 Seconds
(without alignments)
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Title: US-10-541-315-1

Perfect score: 2195
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Scoring tables: **OLIGO_NUC**
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 8

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

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1: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	1267	57.7	14203	AF294979	AF294979 Binary ve
5	1267	57.7	14230	AF294980	AF294980 Binary ve
6	1266	57.7	3192	OSGOS2G	X51910 O. sativa (r
7	1168	53.2	105692	AP003953	AP003953 Oryza sat
8	1168	53.2	110000	AP008213_206	Continuation (207
9	1168	53.2	144741	AP004674	AP004674 Oryza sat
10	1165	53.1	3032	CQ895917	CQ895917 Sequence
11	936	42.6	2191	CS055056	CS055056 Sequence
12	402	18.3	898	AR643981	AR643981 Sequence
13	402	18.3	898	AX044095	AX044095 Sequence
14	402	18.3	898	AX044183	AX044183 Sequence
15	69	3.1	752	AK120697	AK120697 Oryza sat
16	65	3.0	744	AF094774	AF094774 Oryza sat
17	65	3.0	1275	AK105037	AK105037 Oryza sat
18	37	1.7	773	AF380357	AF380357 Porteresi

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20	29	1.3	48	6	AX044062	Sequence
21	29	1.3	48	6	AX044162	Sequence
22	27	1.2	12733	6	AX344992	Sequence
23	25	1.1	21631	8	AC005332	Sequence
24	25	1.1	254308	14	AC103498	Sequence
25	24	1.1	24	6	AX576643	Sequence
26	24	1.1	24	6	AX576644	Sequence
27	24	1.1	2872	2	DDIURBPB	Sequence
28	24	1.1	37057	15	AC149333	Sequence
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30	24	1.1	153751	2	AC116551	Dicysteine
31	24	1.1	157943	15	AP003443	Oryza sat
32	24	1.1	158830	15	AP003372	Oryza sat
33	24	1.1	1221574	14	AC098111	Rattus no
34	24	1.1	1225352	14	AC123312	Rattus no
35	24	1.1	1226979	14	AC128140	Rattus no
36	24	1.1	1227958	14	AC105532	Rattus no
37	24	1.1	1231583	5	CR383672	Zebrafish
38	24	1.1	244424	14	AC131614	Rattus no
39	24	1.1	1252743	14	AC098928	Rattus no
40	24	1.1	1254519	14	AC106458	Rattus no
41	24	1.1	1260838	14	AC130235	Rattus no
42	24	1.1	1292390	14	AC105677	Rattus no
43	23	1.0	4592	15	AK100568	Oryza sat
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ALIGNMENTS

RESULT 1	CQ876145	2195 bp	DNA	linear	PAT 04-OCT-2004
LOCUS	CQ876145	Sequence 1 from Patent WO2004065596.			
DEFINITION	CQ876145				
ACCESSION	CQ876145.1	GI:53789748			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Oryza sativa				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.				
REFERENCE	1	Hatzfeld, Y. and Inze, D.			
AUTHORS					
TITLE	Regulatory sequence				
JOURNAL	Patent: WO 2004065596-A 1 05-AUG-2004;				
	CropDesign N.V. (BE)				
FEATURES	Location/Qualifiers				
source	1..2195				
	/organism="Oryza sativa"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:4530"				
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Query Match	100.0%;	Score 2195;	DB 6;	Length 2195;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 2195;	Conservative	0;	Mismatches	0;	Indels
0;	Gaps	0;			
Oy	1	AATCGAAAAGTTTGACGCGTTTTCAGTCCTTAACATACATATAGGAAAGTGTGCT	60		
Db	1	AATCGAAAAGTTTGACGCGTTTTCAGTCCTTAACATACATATAGGAAAGTGTGCT	60		
Oy	61	AAATATAAATGAGACCTTAATATATGTCGCGTGAATACATGAATTAAGTAAAGAAACT	120		
Db	61	AAATATAAATGAGACCTTAATATATGTCGCGTGAATACATGAATTAAGTAAAGAAACT	120		
Oy	121	CATCAGCCTACTTTGTGCGAATCGGCTAAATATAAAGAGTGCCTACAGTTTGGT	180		
Db	121	CATCAGCCTACTTTGTGCGAATCGGCTAAATATAAAGAGTGCCTACAGTTTGGT	180		
Oy	181	TTTCCTAGTATATTAAGTGGAAATGAATCATTTATGCTTAGAATATACGTTCAATC	240		

Db 181 |TTCTCTAGTAATTAAGTGGGAAAATGAATCATATATGCTTAAGATATACGTTCAATC| 240
 Qy 241 |TCTGTCATGAAAGTTAAATTAATTCGAGTAGCCATTAATTCATCAAACTCTTCTGATA| 300
 Db 241 |TCTGTCATGAAAGTTAAATTAATTCGAGTAGCCATTAATTCATCAAACTCTTCTGATA| 300
 Qy 301 |AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAT| 360
 Db 301 |AAAAAATCTTCTAGCTGAACCTCAATGGGTAAAGAGATATTTTTTTTTTAAAAAAT| 360
 Qy 361 |AGAAATGAATATTCGAAAGATATCGGCAAAAGTTTAAACATTAATTAATTAATTTTAT| 420
 Db 361 |AGAAATGAATATTCGAAAGATATCGGCAAAAGTTTAAACATTAATTAATTAATTTTAT| 420
 Qy 421 |AGTTTGTGCAATCGTATATCGCAGTCATTAAGAGATGTCCTTACATCTCAATTTT| 480
 Db 421 |AGTTTGTGCAATCGTATATCGCAGTCATTAAGAGATGTCCTTACATCTCAATTTT| 480
 Qy 481 |TATTTAGTAATTAAGACAATGACCTTAATTTTTTATTTATCTTTTTTGAATTAGATGC| 540
 Db 481 |TATTTAGTAATTAAGACAATGACCTTAATTTTTTATTTATCTTTTTTGAATTAGATGC| 540
 Qy 541 |AAGGTAATTAAGACAATGACCTTTGTGCTCATGTGCAATGTGAGTGCACTCTCTCAATAC| 600
 Db 541 |AAGGTAATTAAGACAATGACCTTTGTGCTCATGTGCAATGTGAGTGCACTCTCTCAATAC| 600
 Qy 601 |GTTCAACTAGCGACATCTCCAAATATCACTCGCTAATTTAATACATTTAGGAGATAT| 660
 Db 601 |GTTCAACTAGCGACATCTCCAAATATCACTCGCTAATTTAATACATTTAGGAGATAT| 660
 Qy 661 |TCTGAATTAAGACAATGACCTTCAACAGACCACTTTAATATATCTAAATACAAAA| 720
 Db 661 |TCTGAATTAAGACAATGACCTTCAACAGACCACTTTAATATATCTAAATACAAAA| 720
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 Db 781 |AAAAAATGAATTTTGTGCTGAGCGAGGAGCCAACTCCCAATTTAGGAGACAGGCAAA| 840
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 Db 841 |CAACAGAGTGGCTGCCACAGAACCAACCAAAAAACGATGATCTAAACGAGAGACAGCA| 900
 Qy 901 |AGTCCGCAACAACTTTTAAACAGCAGGCTTTGGGCAAGAGAGAGAGAGAGAGGCAAG| 960
 Db 901 |AGTCCGCAACAACTTTTAAACAGCAGGCTTTGGGCAAGAGAGAGAGAGAGAGGCAAG| 960
 Qy 961 |AAAAACAAGCATCTCTCTCCCATCTAATAATTCCTCCCTTTTCCCTCTCTATA| 1020
 Db 961 |AAAAACAAGCATCTCTCTCCCATCTAATAATTCCTCCCTTTTCCCTCTCTATA| 1020
 Qy 1021 |TAGAGGCAATCCAGAGCAAGAGAGAGAGAGACCAAGAGACAGCAGCTTAGAGAGAGCGG| 1080
 Db 1021 |TAGAGGCAATCCAGAGCAAGAGAGAGAGAGAGACCAAGAGACAGCAGCTTAGAGAGAGCGG| 1080
 Qy 1081 |AGCGACCGCTTCTTGCATCATATCTTCGGTCGATCTCTTGTGCAATCTCTCCCTCC| 1140
 Db 1081 |AGCGACCGCTTCTTGCATCATATCTTCGGTCGATCTCTTGTGCAATCTCTCCCTCC| 1140
 Qy 1141 |TCACCTCTCTCCACAGGAGTATGAGCCCTGCGTGTCTTGAGATTAATGTTCTAGGT| 1200
 Db 1141 |TCACCTCTCTCCACAGGAGTATGAGCCCTGCGTGTCTTGAGATTAATGTTCTAGGT| 1200
 Qy 1201 |TGTGTAGTACGAGGCGTTGTATGTAGGAAAGGGAGATCTGTATCTGTGATATCTGTTCT| 1260
 Db 1201 |TGTGTAGTACGAGGCGTTGTATGTAGGAAAGGGAGATCTGTATCTGTGATATCTGTTCT| 1260
 Qy 1261 |TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGGTTTGGTTGATAGTAT| 1320
 Db 1261 |TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGGTTTGGTTGATAGTAT| 1320

Db 1261 |TGGATTTGGGATAGAGGGGTTCTTGATGTTGCAATGTTATCGGTTTGGTTGATAGTAT| 1320
 Qy 1321 |ATGCTTTTCAATCGTCTGAGAGCTCTATGAAATGAATAGTTTAAAGGTAACGAATCTT| 1380
 Db 1321 |ATGCTTTTCAATCGTCTGAGAGCTCTATGAAATGAATAGTTTAAAGGTAACGAATCTT| 1380
 Qy 1381 |GGGATTTTGTAGATACCTTTTGTGAGGTAAATCAGAGCACCGGTATATTTGCTTGGT| 1440
 Db 1381 |GGGATTTTGTAGATACCTTTTGTGAGGTAAATCAGAGCACCGGTATATTTGCTTGGT| 1440
 Qy 1441 |GTAATAAAGTATGATTTGTTGCTCGATTTCTGATGATGATGCTTCTCGATTTGACGA| 1500
 Db 1441 |GTAATAAAGTATGATTTGTTGCTCGATTTCTGATGATGATGCTTCTCGATTTGACGA| 1500
 Qy 1501 |AGCTATCTTGTATTTCCCTATTTGAACAAATAATCAACTTTGAAAGACGCTCCGT| 1560
 Db 1501 |AGCTATCTTGTATTTCCCTATTTGAACAAATAATCAACTTTGAAAGACGCTCCGT| 1560
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 Qy 1681 |TCCCTGTTCTTCCGATTTGTAGTCCAGAAATTTTTTCCCAATATCTTAAAAAGT| 1740
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 Qy 1741 |CACTTTCGTTGATGATTAATGAATGATTTGTGCAATTAATGCTTTATAGCTTATCC| 1800
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 Db 1801 |TAGCTGATGTTCAATTTATAGGTAATACCCATATGTTAGTACAGAGAGAACTTATCC| 1860
 Qy 1861 |GATTTCTGATCTCCATTTTATTAATTAATGAATGAACGTGATGACAGATTCATTT| 1920
 Db 1861 |GATTTCTGATCTCCATTTTATTAATTAATGAATGAACGTGATGACAGATTCATTT| 1920
 Qy 1921 |GGATTAATTTTATTAATGCTTTACCCCTTCATTTCTGAGCTGAAAGTCTGGCATGA| 1980
 Db 1921 |GGATTAATTTTATTAATGCTTTACCCCTTCATTTCTGAGCTGAAAGTCTGGCATGA| 1980
 Qy 1981 |ACTGTCCTCAATTTGTTTCAAAATTCATGATTAATCTATPCGATTAATCTCTGTATTC| 2040
 Db 1981 |ACTGTCCTCAATTTGTTTCAAAATTCATGATTAATCTATPCGATTAATCTCTGTATTC| 2040
 Qy 2041 |TACCTGTAGAAATTTCTTTTGTGTTATCTTGAACGTGCTGATTAACAGAAAGAAATTTAT| 2100
 Db 2041 |TACCTGTAGAAATTTCTTTTGTGTTATCTTGAACGTGCTGATTAACAGAAAGAAATTTAT| 2100
 Qy 2101 |GAACTGTAAATCGGAGATGTTATCTGCTTGTCTTAATGATTAATTCCTTTGTGAGTT| 2160
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RESULT 2
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 LOCUS BD251965 Artificial matrix attachment region for increasing expression of
 DEFINITION genes introduced in plant cells.
 ACCESSION BD251965
 VERSION BD251965.1 GI:33061735
 KEYWORDS JP 2002531097-A/27.
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE other sequences; artificial sequences.
1 (bases 1 to 9361)
AUTHORS Geest,A.H.V.D., Ainley,M.W., Cowen,N.M., Welter,M.B. and
Woosley,A.T.
TITLE Artificial matrix attachment region for increasing expression of
genes introduced in plant cells
JOURNAL Patent: JP 2002531097-A 27 24-SEP-2002;
DOM AGROSCIENCES LLC
COMMENT OS Artificial Sequence
PN JP 2002531097-A/27
PP 24-SEP-2002
PP 30-NOV-1999 JP 2000585431
PR 01-DEC-1998 US 60/110437
PI APOLOJIA HM VAN DER GEBST, MICHAEL W AINLEY, NEIL M COWEN, MARY E
WELTER.
PI AARON T WOOSLEY
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC
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ORIGIN
Query Match 57.7%; Score 1267; DB 6; Length 9361;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 683 TCACGAGACCACTTTAATATATCTAAATACAAAATTAATTTTACAGATAGCATGA 742
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DB 6292 GCGCGAGCGCAATCTCCATATTTGGGACACAGGCAACAGAGTGGTGGCCACAGA 6233
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DB 6232 ACAACCCACAAAAGATGATCTAAACGAGGACAGCAAGTCCGCAACCACTTTTAACA 6173
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DB 6172 GCAGGCTTTGCGCCAGAGAGAGAGAGGCAAGAAACCAAGCATCTCTCTCTC 6113
QY 983 CCACTATATAATTCCTCCCTTTTCCCTCTCTATATAGGAGCATCCAAGCAAGAA 1042
DB 6112 CCACTATATAATTCCTCCCTTTTCCCTCTCTATATAGGAGCATCCAAGCAAGAA 6053
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DB 6052 GAGGAGAGACCAAGAGACGCGACTAGAGAGAGCGAGCGCGCTTCTTGATCCA 5993
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DB 5992 TATCTTCGCGTTCGAGTCTTGATCTTCCTCTCTCACTCTCTCTCAAGGATA 5933
QY 1163 TGTGCGCTTGGTTGTTCTTGATTTATTTCTAGGTTGTAGTACGGGCGTTGATGT 1222
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QY 1283 TTGATCTGCATGTTATCGGTTCCGTTGATAGTATGATGATTTCAATCGCTGGAGA 1342
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QY 1943 TCACCCCTTCATTTATCTGAGCTGAAGTCTGGATGAACCTGCTCAATTTTGTTCGA 2002
DB 5152 TCACCCCTTCATTTATCTGAGCTGAAGTCTGGATGAACCTGCTCAATTTTGTTCGA 5093
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QY 2123 TACTGCTGTTCTTATGATTCATTTCTTGTGAGAGTTCTTGATGCTTCCACTTTC 2182
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QY 2183 ACCAGCAAAAGTTC 2195
DB 4912 ACCAGCAAAAGTTC 4900

RESULT 3
BD251966/c BD251966 10629 bp DNA linear PART 17-UTL-2003
LOCUS
DEFINITION Artificial matrix attachment region for increasing expression of

ACCESSION	BD251966	Genes introduced in plant cells.
VERSION	BD251966.1	GI:33061736
KEYWORDS	JP 2002531097-A/28.	
SOURCE	Synthetic construct	
ORGANISM	Synthetic construct	
REFERENCE	other sequences; artificial sequences. 1 (bases 1 to 10629)	
AUTHORS	Geeis,A.H.V.D., Ainley,M.W., Cowen,N.M., Welter,M.E. and Woosley,A.T.	
TITLE	Artificial matrix attachment region for increasing expression of genes introduced in plant cells	
JOURNAL	Patent: JP 2002531097-A 28 24-SEP-2002; DOW AGROSCIENCES LLC	
COMMENT	OS Artificial Sequence PN JP 2002531097-A/28 PD 24-SEP-2002 JP 2000585431 PF 30-NOV-1999 JP 2000585431 PR 01-DEC-1998 US 60/110437 PI ABOLONIA HM VAN DER GEEST,MICHAEL W AINLEY,NEIL M COWEN,MARY E	
FEATURES	source location/Qualifiers /organism='Artificial Sequence'. FT source 1..10629	
ORIGIN	PI WOOLEY, PI AARON T WOOLEY PC CI2N15/09,AOIH5/00,CI2N5/10,CI2N15/00,CI2N5/00 CC Description of Artificial Sequence:patGOS2af-hpt FH Key Location/Qualifiers FT source 1..10629 location/Qualifiers 1..10629 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"	
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Best Local Similarity	99.6%; Pred. No. 0;	Mismatches 6; Indels 0; Gaps 0;
Matches 1567; Conservative	0;	
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Oy	663 TCACGAGACCCTTTAATAATATCTAATAATACAAAAATAATTTTACAGAATATGCATGA	742
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Db	6991 AAAGTATGAAGCACTAATTTAGTTTTTCACATACAAAATAATTTTGCTCGT	69922
Oy	803 GCGGAGGCGCAATCTCCCATATTTGGGACAACAGGCAACAACAGGTGGCTGCCACAGA	862
Db	6931 GCGGAGGCGCAATCTCCCATATTTGGGACAACAGGCAACAACAGGTGGCTGCCACAGA	6872
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Db	6871 ACAACCCCAAAAAACGATGATCTTAACGAGACAGCAAGTCCGCAACAACCTTTTACA	6812
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Db	6811 GCAGGCTTTGGGCGCACAGAGAGAGAGAGAGCAAGAAAAACAAGCATCTCTCCTC	67522
Oy	983 CCATCTTAATAATTTCTCCCCCTTTTCCCCTCTCTATATAGAGGCATCCAAAGCAAGA	1042
Db	6751 CCATCTTAATAATTTCTCCCCCTTTTCCCCTCTCTATATAGAGGCATCCAAAGCAAGA	66922
Oy	1043 GAGGAGAGACCAAGACAGCGACTGACGAAGAAGCCGAGGACCGCTTTCTTGATCCA	1102
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Db	6631	TATCTCCGGTCGACGTTCTTGGTGCATCTCTTCCTCCTCCACCTCCTCTCACAGGGTA	6572
Qy	1163	TGTGCCCTTCGGTGTGTTCTTGGATTATATGTTCTTACGTGTGTAGTACGGGCGTTGATGT	1222
Db	6571	TGTGCCCTTCGGTGTGTTCTTGGATTATATGTTCTTACGTGTGTAGTACGGGCGTTGATGT	6512
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Db	6511	TAGGAAAGGGATCTGTATCTGTGTATGATTTCTGTCTTGGATTGGGATAGAGGGCTTC	6452
Qy	1283	TTGATGTGCAGTGTATGTTCCGTTGATTAGTAGTATGTTTCAATGCTCGAGAGA	1342
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Qy	1403	TTTGAAGTAAATCAGAGCACCGGTGATTTTGTGTGTATATAAGTACATTGTTTG	1462
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Qy	1463	GTCCCTCGATTCGGTAGTATGCTTCTCGATTGACGAAAGCTATCCTTGTATATCCCT	1522
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Qy	1703	TAGTCCCGAATTTTTTTCCCAATATCTTAAAGAGTCACTTTCGTGTCAGTTCATG	1762
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Db	5671	GTTATATCTTGACGTCTGATTACAGAAAGAAATTTATGAAGCTGTATCCGGATATGTTA	5612
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Db	5551	ACCAAGCAAGTTC 5539	

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1917 TAAATACCCCTATAGTTAGTACGAGAGAAAGTATCCGATTTCCGATTTTAA 1976
1943 TAAATACCCCTATAGTTAGTACGAGAGAAAGTATCCGATTTCCGATTTTAA 2002
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Db 2217 ACCAGCAAGTTTC 2229
RESULT 5
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LOCUS Binary vector pINDEX2, complete sequence.
DEFINITION AF294980
ACCESSION AF294980.1 GI:11559666
VERSION AF294980.1
KEYWORDS
SOURCE
ORGANISM
BINARY VECTOR pINDEX2
BINARY VECTOR pINDEX2
OTHER SEQUENCES: artificial sequences; vectors.
REFERENCE
1 (bases 1 to 14230)
Ouwkerk, P.B., de Kam, R.J., Hoge, J.H. and Meijer, A.H.
Glucocorticoid-inducible gene expression in rice
Planta 213 (3), 370-378 (2001)
JOURNAL
PUBMED
11506359
REFERENCE
2 (bases 1 to 14230)
Ouwkerk, P.B.F.
Direct Submission
Submitted (11-AUG-2000) Dept. of Molecular Cell Biology, Institute
for Molecular Plant Sciences, Wageningen 64, Leiden 2333 AL,
Netherlands
COMMENT
pINDEX2 is a binary vector designed for glucocorticoid-inducible
gene expression in plants and is optimized for use in rice; pINDEX2
is part of a series of four pINDEX vectors (Genbank Accession
Numbers AF294979-AF294982). pINDEX vectors are based on parts of
pCAMBIA-1300 encoded by Genbank Accession Number AF234296 and
pTA7002 (Toyama, T. and Chua N.-H., 1997, Plant J. 11:605-612).
FEATURES
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intron
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QY 1883 TTATATGAATGAACGTATAGCATATGACATATCTTGGATTTATTTTATTAAGCTT 1942
DB 1917 TTATATGAATGAACGTATAGCATATGACATATCTTGGATTTATTTTATTAAGCTT 1976
QY 1943 TCACCCCTTCATTTATCTGAGCTGAAAGTCTGCGATGAACGTCTCAATTTGTTTCA 2002
DB 1977 TCACCCCTTCATTTATCTGAGCTGAAAGTCTGCGATGAACGTCTCAATTTGTTTCA 2036
QY 2003 AATTGACATCGATTTATCTATGATATATCTCTGATGATGATGATGATGATGATGAT 2062
DB 2037 AATTGACATCGATTTATCTATGATATATCTCTGATGATGATGATGATGATGATGAT 2096
QY 2063 GTTATTTCTTGACTGCTGATTTACAGAAAGAAATTTATGAAGCTGTAATCCGGATATGTA 2122

Db	2097	GTATTTCTTACCTGCTTGAATTACGAAAGAAATTTATGAAAGCTATATCGGATAGTTA	2156
Qy	2123	TACTGCTTGTCTTATGATGATCATTTCTTTGTGACGTTCTTGTTGACCTTGCCACTTTC	2182
Db	2157	TACTGCTTGTCTTATGATGATCATTTCTTTGTGACGTTCTTGTTGACCTTGCCACTTTC	2216
Qy	2183	ACCAGCAAAAGTTC	2195
Db	2217	ACCAGCAAAAGTTC	2229
RESULT 6			
LOCUS	OSGOS2G	3192 bp	DNA
DEFINITION	O. sativa (rice) constitutive GOS2 gene.	linear	PLN 18-APR-2005
ACCESSION	X51910		
VERSION	X51910.1	GI:20237	
KEYWORDS	GOS2 gene; rice.		
SOURCE	Oryza sativa (indica cultivar-group)		
ORGANISM	Oryza sativa (indica cultivar-group)		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;		
	Ehretidoideae; Oryzeae; Oryza.		
REFERENCE	1		
AUTHORS	de Pater,B.S., van der Mark,F., Rueb,S., Katagiri,F., Chua,N.H.,		
	Schilperoort,R.A. and Hengsem,L.A.		
TITLE	The promoter of the rice gene GOS2 is active in various different		
	monocot tissues and binds rice nuclear factor ASF-1		
JOURNAL	Plant J. 2 (6), 837-844 (1992)		
PUBMED	1302635		
REFERENCE	2 (bases 1 to 3192)		
AUTHORS	de Pater,B.S.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-FEB-1990) De Pater B.S., Center for Phytotechnology		
	RUN/TNO, Dept. of Plant Mol. Biol., Nomensteeg 3, 2311 VJ Leiden,		
	The Netherlands		
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Best Local Similarity	99.6%; Pred. No. 0;	
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Oy	683 TCACCAAGCACCTTTTAAATATCTAAATACAAAAATTAATTTTACAGAATAGCATGA	742
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Oy	863 ACAACCCACAAAAACGATGATCTTAACGGAGAACAGCAAGTCCGCAACAACCTTTTAA	922
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Oy	983 CCAATCTAATATCTCTCCCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1042
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Oy	557	CACATTGGGCTCATGTGCATGTGTGAGTGACCGCTCC-ATACAGGTTCAACTAGGCACA	615
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Oy	736	AGCATGAAAAGTATGAAGCAACATATTAGTTTTTCACATACAAAAAATTAAGAAATTT	795
Db	22171	AGCATGAAAAGTATGAAGCAACATATTAGTTTTTCACATACAAAAAATTAAGAAATTT	22112
Oy	796	TGCTCTGTGCGGAGACGCGCAATCTCTCCATATTGGGACACAGGCAACACAGAGTGCGTGC	855
Db	22111	TGCTCTGTGCGGAGACGCGCAATCTCTCCATATTGGGACACAGGCAACACAGAGTGCGTGC	22052
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Db	21871	CCAAAGAAAGGAGAGACCAAGAGACACGCGACTAGACAGAAAGCGACGACGCGCGC-TCCT	21813
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Oy	1156	CAGGGTATATG- --CCCTCGGTTGTCCTTGGAATTAATTTCTAGATTGTGATGACGG	1212
Db	21752	CAGGGTATATGCTCTCCCTCGGTTGTCTTGAATTTATTTCTTAGATTGTGATGACGG	21693
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Db	21692	GCGTTGATGTTAGAAAGGGGATCTGTATCTGTAGATATTCCTGTTCTTGAAATTTGGAA	21633
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Db	21632	AGAGGGGTTCTTGATGTTGCATGTTATCGGTTGGGTTGATTAGTAGATAGTTTCAAT	21573
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Db	21572	CGTCTGAGAGACTTATAGAAATGAATAGTTTAAGGATTCGGAATCTTGCGAATTTTGTA	21513
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Db	21512	GTACCTTTTGTGAGGTAATAACAGACACCGGTATTTTGCTGTGTGTAAT-AAAAGTA	21454
Oy	1453	CATTGTGTGCTCGATTCGTGTGATGATGCTTCTGATTTGACGAAGCTATCTCTTG	1512

Db	21453	CATTGTTGGTGCTCGATTCCTGTAAGTAGTGCTTCTCGATTGTGACGAAGCATCCTTTG	21394
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Db	21393	TTTATTTCCCAATTGAAACAAATAATATCAACCTTTGAAGACGGTCCCGTTGATGAGATTGA	21334
Qy	1513	ATGATTTGATTTCTTAAGCTGTCCAAAATTTTCGAGCTGGCTGTTTAAATAAGTAGTCC	1632
Db	21333	ATGATTTGATTTCTTAAGCTGTCCAAAATTTTCGAGCTGGCTGTTTAAAGTAGTAGTCC	21274
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Qy	1933	TTATTTAGCTTTCAACCCCTCATTTATTTCTGAGCTGAAAGTCTGGCATGAACCTGCTCAAT	1992
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Qy	1993	TTTGTCTTTGAAATTCACATGATTAATCTATCGATTCATCCCTTGATCTACACGTGAGAAAG	2052
Db	20913	TTTGTCTTTGAAATTCACATGATTAATCTATCGATTCATCCCTTGATCTACACGTGAGAAAG	20854
Qy	2053	TTTGTCTTTGATTAATTCCTGATCTGCTGTATTCAGAAAGAAATTTATGACGTGTATTC	2112
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RESULT 8
AP008213 206/c
WPCOMMENT

Sequence split into 297 fragments. LOCUS AP008213 Accession AP008213

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Qy	1273	AGAGGGGTCTTGATGTTGCAATGTTATCGGTTTGGTTTGAATTAGTAGTATGTTTTCAAT	1332
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RESULT 9
AP004674/c 144741 bp DNA linear PLN 22-JUL-2004
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,
DEFINITION PAC clone: P0681F05.
ACCESSION AP004674
VERSION AP004674
KEYWORDS GI:26017274
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriocaridaceae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nupponbare (GA3) genomic DNA, chromosome 7, PAC
clone: P0681F05
JOURNAL Published Only in Database (2002)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Substitution
JOURNAL Submitted (23-JAN-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasakit@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On Dec 3, 2002 this sequence version replaced gi:18307752.
Gene were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), GENESH
(http://www.softberry.com/), GeneMark_hmm
(http://opal.biology.gatech.edu/GeneMark/), Glimmer3

FEATURES

source

(http://www.tigr.org/tdb/glimmer3/glimmer3_form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplinePredictor
(http://bioinformatics.lasstate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim.html), gap2
(http://www.tigr.org/software/glimmer/). BLASTN and BLASTX. The
genomic sequence was searched against NCBI Nonredundant protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DBJ. Protein homologues of the coding
regions were searched against NCBI Nonredundant protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as
a probable 'hypothetical' protein and is included as a
miscellaneous feature of the sequence.
The orientation of the sequence is from 5' to 3' of the PAC clone.
This sequence of P0681F05 clone has an overlap with OSJNB004712
(DBJ: AP004990) clone at 5' end and with OSJNB0044C15 (DBJ:
AP005850) at 3' end. Detailed information on overlap and assembly
quality together with annotation of this entry is available at
http://rgp.dna.affrc.go.jp/Genomeseg.html.
Location/Qualifiers

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/cultivar="nupponbare"

/db_xref="taxon:39947"

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Best Local Similarity 99.4%; Pred. No. 0;
Matches 2168; Conservative 0; Mismatches 8; Indels 6; Gaps 4;
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DEFINITION CQ895917
ACCESSION CQ895917
VERSION CQ895917.1 GI:55467905
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SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 sanz Molinero, A.I.
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TITLE the same
JOURNAL Patent: WO 2004090142-A 7 21-OCT-2004;
CropDesign N.V. (BE)
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Db	1041	GAGGAGAGGACACAAAGGACACGGCGACTAGACAGAACCGAGGAGCCGCTCTTCGATCCA	1100
QY	1103	TATCTTCCGGTCCGAGTCTTTGGTCGATCTTCCCTCCACCTCTCCACAGGCTA	1162
Db	1101	TATCTTCCGGTCCGAGTCTTTGGTCGATCTTCCCTCCACCTCTCCACAGGCTA	1160
QY	1163	TGTGCGCTTCCGGTCTTCTTGATTTATTTGTTCTTAGGTTGTGTAGTACGGCGCTTATGT	1222
Db	1161	TGTGCGCTTCCGGTCTTCTTGATTTATTTGTTCTTAGGTTGTGTAGTACGGCGCTTATGT	1220
QY	1223	TAGGAAAGGGGATCTGTATCTGTAGTATTCCTGTCTTGATTTGGGATAGAGGGGTTT	1282
Db	1221	TAGGAAAGGGGATCTGTATCTGTAGTATTCCTGTCTTGATTTGGGATAGAGGGGTTT	1280
QY	1283	TTGATGTTCAGTGTATTCGGTTCGGTTTGATTTAGTATGATGATTTTCAATCGTCTGAGA	1342
Db	1281	TTGATGTTCAGTGTATTCGGTTCGGTTTGATTTAGTATGATGATTTTCAATCGTCTGAGA	1340
QY	1343	GCTCTATGAAATGAATAGTGTTAGGGTACGGAAATCTTGCGATTTTGTAGTACCTTTTG	1402
Db	1341	GCTCTATGAAATGAATAGTGTTAGGGTACGGAAATCTTGCGATTTTGTAGTACCTTTTG	1400
QY	1403	TTTGAGGTAAATACGACACCGGATTTTGTCTGGGTAAATAAGTACATTTGTTTG	1462
Db	1401	TTTGAGGTAAATACGACACCGGATTTTGTCTGGGTAAATAAGTACGATTTGTTTG	1460
QY	1463	GTCCTCGATTCGAGTAGATGCTTCTCGATTTTGACGAAGCTATCTTTGTTTATCCCT	1522
Db	1461	GTCCTCGATTCGAGTAGATGCTTCTCGATTTTGACGAAGCTATCTTTGTTTATCCCT	1520
QY	1523	ATTGAACAAAAATAATCAACTTTGAGAACGGTCCGTTGATGAGATTGAATGATTTGAT	1582
Db	1521	ATTGAACAAAAATAATCAACTTTGAGAACGGTCCGTTGATGAGATTGAATGATTTGAT	1580
QY	1583	CTTAAGCCTGTCCAAAAATTTGGCAGCTGGCTTTGTATACATACATAGTCCCATCAAGAA	1642
Db	1581	CTTAAGCCTGTCCAAAAATTTGGCAGCTGGCTTTGTATACATACATAGTCCCATCAAGAA	1640
QY	1643	ATTCAATGAAACAGTTATTAATCTCTACAGAAACAGGGGATTCCTGTCTCTCCGATTTGCT	1702
Db	1641	ATTCAATGAAACAGTTATTAATCTCTACAGAAACAGGGGATTCCTGTCTCTCCGATTTGCT	1700
QY	1703	TAGTCCCGAATTTTTTTTCCCAATATCTTAAAAAGTCACTTTCTGGTTCAGTTCAATG	1762
Db	1701	TAGTCCCGAATTTTTTTTCCCAATATCTTAAAAAGTCACTTTCTGGTTCAGTTCAATG	1760
QY	1763	AATTGATTGCTACAAATATATGCTTTTATAGCGTTATCTTAGCTGTAGTTCAGTTTATAGG	1822
Db	1761	AATTGATTGCTACAAATATATGCTTTTATAGCGTTATCTTAGCTGTAGTTCAGTTTATAGG	1820
QY	1823	TAATAACCCCTATAGTTTAGTACAGAGGAAAGAACTTACGATTTCTGATCTCCATTTTAA	1882
Db	1821	TAATAACCCCTATAGTTTAGTACAGAGGAAAGAACTTACGATTTCTGATCTCCATTTTAA	1880
QY	1883	TTAATATGAAATGAACGTGATGATTAAGCATATTCATTTGATTTATTTTATTTATAGCTT	1942

Db	1861	TTATATGAAATGAACCTGAGCATAGACGATATCATTTGGATTATTTTTTTTATTAAGCTC	1940
QY	1943	TCACCCCTTCATTAATTCGAGCTGAAGATCTGGACATGAACATGTCCTCAATTTGTTTTCA	2002
Db	1941	TCACCCCTTCATTAATTCGAGCTGAAGATCTGGACATGAACATGTCCTCAATTTGTTTTCA	2000
QY	2003	AATTCACATGCATTATCTATGCATTATTCCTTTGTATCTACCTGTAGAAGTTTCTTTTGG	2062
Db	2001	AATTCACATGCATTATCTATGCATTATTCCTTTGTATCTACCTGTAGAAGTTTCTTTTGG	2060
QY	2063	GTTATTCCTTGACCTGCTGATTACAGAAAGAAATTTATGAAGCTGTAATCGGATAGTTA	2122
Db	2061	GTTATTCCTTGACCTGCTGATTACAGAAAGAAATTTATGAAGCTGTAATCGGATAGTTA	2120
QY	2123	TACTGCTGTGTTCTTATGATTCATTTCTTTGTGAGATTCCTGTGATGCTTGCCACATTTTC	2182
Db	2121	TACTGCTGTGTTCTTATGATTCATTTCTTTGTGAGATTCCTGTGATGCTTGCCACATTTTC	2180
QY	2183	ACCAAGCAAAAGTTTC	2195
Db	2181	ACCAAGCAAAAGTTTC	2193

RESULT 11				
CS055056	CS055056	2191 bp	DNA	Linear
LOCUS	Sequence 15 from Patent WO2005024029.			
DEFINITION	CS055056			
ACCESSION	CS055056.1	GI:62121528		
VERSION				

KEYWORDS .
SOURCE *Oryza sativa*

ORGANISM *Oryza sativa*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzaceae; Oryza.

REFERENCE AUTHORS TITLE
1 Broekseert, W., Frankard, V., Hatzfeld, Y. and Mironov, V. Plants having modified growth characteristics and method for making the same

JOURNAL	Patent : WO 2005024029-A-15 17-MAR-2005 ; CropDesign N.V. (BE)
FEATURES	Location/Qualifiers
SOURCE	1. .2191

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ORIGIN
/organism="Oryza sativa"
/mol_type="unassigned DNA"
/db_xref="taxon:4530"

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Query Match	42.6%	Score 936	DB 6	Length 2191
Best Local Similarity	99.5%	Pred. No. 0		
Matches 1306; Conservative	0	Mismatches 5	Indels 1	Gaps 1

[illegible]

Qy	683	TCACCAGACCACTTTTATATAATCTAATAATACAAAATAATTTTACAGATGATGA	742
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Oy 743 AAGATGAAACGACTATTAGTTTTCACATCAAAAAAAGAAATTTTGCTCGT 802
|||
Db 741 AAAGTAGAACGACTATTAGTTTTTCACATCAAAAAAAAAAGAAATTTTGCTCGT 800

Oy 803 GCGGAGCGCCAAATCTCCATATTGGGCACACAGGCAACAAGTGGTGCCACAGA 862
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 801 GCGGAGCGCCAAATCTCCATATTGGGCACACAGGCAACAAGTGGTGCCACAGA 860

Qy	863	ACAA	CCCA	CAAAAA	CG	TG	TG	TT	CT	TAA	CG	GA	GA	CAG	CA	AG	T	CG	CA	CA	A	CT	T	T	T	A	CA	922
Db	861	ACAA	CCCA	CAAAAA	CG	TG	TG	TT	CT	TAA	CG	GA	GA	CAG	CA	AG	T	CG	CA	CA	A	CT	T	T	T	A	CA	920

QY	923	GCAGGCTTTGCGCCAGAGAGAGAGAGAGGCAAAAGAAAACAAGATCCTCTCTC	982
Db	921	GCAAGCTTTGCGGCCAGAGAGAGAGAGAGGCAAAAGAAAACAAGATCCTCTCTC	980
QY	983	CCATCTATAAATTCCTCCCTTTTCCCTCTCTATAATAGAGGCATCCAAAGCCAGAA	1042
Db	981	CCATCTATAAATTCCTCCCTTTTCCCTCTCTATAATAGAGGCATCCAAAGCCAGAA	1044
QY	1043	GAGGAGAGACACAAAGACACGCCACTAGACAAACCCAGAGACCGCTTCTTGATCCA	1102
Db	1041	GAGGAGAGACACAAAGACACGCCACTAGACAAACCCAGAGACCGCTTCTTGATCCA	1100
QY	1103	TATCTCCGGTGAAGTCTTGTCGATCTTCCCTCCCACTCCCTCTCAAGGGTA	1162
Db	1101	TATCTCCGGTGAAGTCTTGTCGATCTTCCCTCCCACTCCCTCTCAAGGGTA	1160
QY	1163	TGTGCTTCGGTGTCTTGATTTATGTCTAGTGTGTAGTACGGGCGTGTAGT	1222
Db	1161	TGTGCTTCGGTGTCTTGATTTATGTCTAGTGTGTAGTACGGGCGTGTAGT	1220
QY	1223	TAGGAAAGGAGATCTGTATCTGTATGATTCCTGTTCTTGATTTGGATTAAGGGTTT	1282
Db	1221	TAGGAAAGGAGATCTGTATCTGTATGATTCCTGTTCTTGATTTGGATTAAGGGTTT	1280
QY	1283	TTGAGTGTGACATGATCGGTTCGGTTTGAATAGATAGATGTTTCAATGTCAGGA	1342
Db	1281	TTGAGTGTGACATGATCGGTTCGGTTTGAATAGATAGATGTTTCAATGTCAGGA	1340
QY	1343	GCTCATGAGAAATGAATGTTTGAAGGTACGGAATCTTGCGATTTTGAGATCACTTTG	1402
Db	1341	GCTCATGAGAAATGAATGTTTGAAGGTACGGAATCTTGCGATTTTGAGATCACTTTG	1399
QY	1403	TTTGAAGTAAATCAGAGCACCGTGATTTTGTGTGTATATAAAGTACATTTGTTG	1462
Db	1400	TTTGAAGTAAATCAGAGCACCGTGATTTTGTGTGTATATAAAGTACATTTGTTG	1459
QY	1463	GTCCTCGAATCTGAGTAGATGCTCTCGATTTGACAAAGCATTCCTTGTTATTCCT	1522
Db	1460	GTCCTCGAATCTGAGTAGATGCTCTCGATTTGACAAAGCATTCCTTGTTATTCCT	1519
QY	1523	ATTGAACAAAATAATCAACTTTGAAACCGTCCGTTGATAGATTGAATGATTGAT	1582
Db	1520	ATTGAACAAAATAATCAACTTTGAAACCGTCCGTTGATAGATTGAATGATTGAT	1579
QY	1583	CTTAAGCCTGTCCAAATTTGCGAGCTGGCTTGTAGATACAGTAGTCCCATCAGAA	1642
Db	1580	CTTAAGCCTGTCCAAATTTGCGAGCTGGCTTGTAGATACAGTAGTCCCATCAGAA	1639
QY	1643	ATTCAATGAAAACGTTATATATCTCAGAAACAGGGGATTCCTCTGTTCTTCGATTGCT	1702
Db	1640	ATTCAATGAAAACGTTATATATCTCAGAAACAGGGGATTCCTCTGTTCTTCGATTGCT	1699
QY	1703	TAGTCCGAAATTTTTTCCCAATATCTTAAAAAGTCACTTCTGGTCAAGTCAAG	1762
Db	1700	TAGTCCGAAATTTTTTCCCAATATCTTAAAAAGTCACTTCTGGTCAAGTCAAG	1759
QY	1763	AATTGATGCTACAATAATGCTTTTATAGCGTTATCTAGCTGATTCAGTTATAG	1822
Db	1760	AATTGATGCTACAATAATGCTTTTATAGCGTTATCTAGCTGATTCAGTTATAG	1819
QY	1823	TAAATCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCATTTTAA	1882
Db	1820	TAAATCCCTATAGTTTATGTCAGAGAAAGAACTTATCCGATTTCTGATCTCATTTTAA	1879
QY	1883	TTATATGAAGAAGTGTAGATAGACAGTATCTATTGGATTAATTTTTTTT	1934
Db	1880	TTATATGAAGAAGTGTAGATAGACAGTATCTATTGGATTAATTTTTTTT	1931

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Db 751 AACGAACTATTAGGTTTTCATCATCAAAAAAAAAAGAAATTTCTGCTGGCGAGG 810
Qy 812 CCAATCTCCCATTTTGGGCGACAGGCAACACAGAGTGGCTGCCAGAGAACCCAC 871
Db 811 CCAATCTCCCATTTTGGGCGACAGGCAACACAGAGTGGCTGCCAGAGAACCCAC 870
Qy 872 AAAAAACGATGATCTAACGAGGACAGC 899
Db 871 AAAAAACGATGATCTAACGAGGACAGC 898

RESULT 13
AX044095 898 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 50 from Patent WO0066748.
DEFINITION AX044095
ACCESSION AX044095
VERSION AX044095.1 GI:11342973
KEYWORDS
SOURCE
ORGANISM
Oryza sp.
Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1

REFERENCE
AUTHORS Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and
PICKERILL, A.P.
TITLE Herbicide resistant plants
JOURNAL Patent: WO 0066748-A 50 09-NOV-2000;
ZENECA LIMITED (GB)
FEATURES
source
1. 898
Location/Qualifiers
/organism="Oryza sp."
/mol_type="unassigned DNA"
/db_xref="taxon:52841"

ORIGIN

Query Match 18.3%; Score 402; DB 6; Length 898;
Best Local Similarity 99.3%; Pred. No. 8e-198;
Matches 862; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

Qy 33 CTAACTAACATATAGGAAAGCGTGTCTAAATTAATAAGAGCCCTTATATATGTCGCC 92
Db 34 CTAACTAACATATAGGAAAGCGTGTCTAAATTAATAAGAGCCCTTATATATGTCGCC 93
Qy 93 TGTAACTAGAACTATATAGAAAGAACTCATCACTTATAGTGGCAATCGGCTAA 152
Db 94 TGTAACTAGAACTATATAGAAAGAACTCATCACTTATAGTGGCAATCGGCTAA 153
Qy 153 TAAAAAAGAGTGGCTACACTAGTTTGTCTTCTTATAGTAAATGAGAAATGAATC 212
Db 154 TAAAAAAGAGTGGCTACACTAGTTTGTCTTCTTATAGTAAATGAGAAATGAATC 213
Qy 213 ATTATTTGCTTAAGATATACGTTCACTCTGTCTGATGAAGTTAAATTCAGAGTAC 272
Db 214 ATTATTTGCTTAAGATATACGTTCACTCTGTCTGATGAAGTTAAATTCAGAGTAC 273
Qy 272 ATTAATTTGCTTAAGATATACGTTCTTGAATTAATAAATCTTCTAGCTCAATGGGTA 332
Db 274 ATTAATTTGCTTAAGATATACGTTCTTGAATTAATAAATCTTCTAGCTCAATGGGTA 333
Qy 333 AGAGAGATATTTTAAAAAATAAGATGAATATCTGAACGTATCGGCAAG 392
Db 334 AGAGAGATATTTTAAAAAATAAGATGAATATCTGAACGTATCGGCAAG 390
Qy 393 ATTTAAACAT 452
Db 391 ATTTAAACAT 450
Qy 453 AGGACATGCTTACTCATCTCAATTTTATTTAGTAAATTAAGAAATGAGCTTATTT 512
Db 451 AGGACATGCTTACTCATCTCAATTTTATTTAGTAAATTAAGAAATGAGCTTATTT 510

Qy 513 TATTAATTAATCTTTTGGATTAAGTGAAGTACTTAAGCACAACACTTTGTCATGT 572
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Qy 573 GCATGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 631
Db 571 GCATGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 630
Qy 632 CGCCTATTTAAT 691
Db 631 CGCCTATTTAAT 690
Qy 692 CACTTTTAAT 751
Db 691 CACTTTTAAT 750
Qy 752 AACGAATCTATTAGTGTTCATATACAAAAAAGAAATTTTGTCTGTGGCGAGCG 811
Db 751 AACGAATCTATTAGTGTTCATATACAAAAAAGAAATTTTGTCTGTGGCGAGCG 810
Qy 812 CCAATCTCCCATTTTGGGCGACAGGCAACACAGAGTGGCTGCCAGAGAACCCAC 871
Db 811 CCAATCTCCCATTTTGGGCGACAGGCAACACAGAGTGGCTGCCAGAGAACCCAC 870
Qy 872 AAAAAACGATGATCTAACGAGGACAGC 899
Db 871 AAAAAACGATGATCTAACGAGGACAGC 898

RESULT 14
AX044183 898 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 35 from Patent WO0066746.
DEFINITION AX044183
ACCESSION AX044183
VERSION AX044183.1 GI:11343061
KEYWORDS
SOURCE
Oryza sp.
Oryza sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1

REFERENCE
AUTHORS Hawkes, T.R., Warner, S.A., Andrews, C.J., Bachoo, S. and
PICKERILL, A.P.
TITLE Herbicide resistant plants
JOURNAL Patent: WO 0066746-A 35 09-NOV-2000;
ZENECA LIMITED (GB)
FEATURES
source
1. 898
Location/Qualifiers
/organism="Oryza sp."
/mol_type="unassigned DNA"
/db_xref="taxon:52841"

ORIGIN

Query Match 18.3%; Score 402; DB 6; Length 898;
Best Local Similarity 99.3%; Pred. No. 8e-198;
Matches 862; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

Qy 33 CTAACTAACATATAGGAAAGCGTGTCTAAATTAATAAGAGCCCTTATATATGTCGCC 92
Db 34 CTAACTAACATATAGGAAAGCGTGTCTAAATTAATAAGAGCCCTTATATATGTCGCC 93
Qy 93 TGTAACTAGAACTATATAGAAAGAACTCATCACTTATAGTGGCAATCGGCTAA 152
Db 94 TGTAACTAGAACTATATAGAAAGAACTCATCACTTATAGTGGCAATCGGCTAA 153
Qy 153 TAAAAAAGAGTGGCTACACTAGTTTGTCTTCTTATAGTAAATTAAGTGGAAATGAATC 212
Db 154 TAAAAAAGAGTGGCTACACTAGTTTGTCTTCTTATAGTAAATTAAGTGGAAATGAATC 213
Qy 213 ATTATTTGCTTAAGATATACGTTCACTCTGTCAATGAAGTTAAATTTAGAGGTAC 272
Db 214 ATTATTTGCTTAAGATATACGTTCACTCTGTCAATGAAGTTAAATTTAGAGGTAC 273

Oy		273	ATAATGTCATCAAACTCCTTGTAATTAABAAAACCTTTCAGCTGAAGCTCAAAGGGTAA	332	
Dd		274	ATAATGTCATCAAACTCTCTTGTAATTAABAAAACCTTTCAGCTGAAGCTCAAAGGGTAA	333	
Oy		333	AGAGAGATATATTTTTTTAAAAAATAAGAATGAATATTTCTGAACGTATCGGCAAG	392	
Dd		334	AGAGAGATATATTTTTTT---AAAAAATAAGAATGAATATTTCTGAACGTATCGGCAAG	390	
Oy		393	ATTTTAACAATATTAATTAATTAATTTTAATAGTTTGCGCATTTGCTTAATTCGACCGTACTTA	452	
Dd		391	ATTTTAACAATATTAATTAATTAATTTTAATAGTTTGCGCATTTGCTTAATTCGACCGTACTTA	450	
Oy		453	AGGACATGCTCACTCCGCAATCTCAATTTTATTAATTAATTAAGAACAATGACTTATTTT	512	
Dd		451	AGGACATGCTCACTCCGCAATCTCAATTTTATTAATTAATTAAGAACAATGACTTATTTT	510	
Oy		513	TATTAATTAATCTTTTTCGATTAGATGCAAGGTAATTAACGACACACTTTTGCTCATGT	572	
Dd		511	TATTAATTAATCTTTTTCGATTAGATGCAAGGTAATTAACGACACACTTTTGCTCATGT	570	
Oy		573	GCAATGTGAGTGCACCCTTCCTC-ATACACGTTTCAACTAGCCACACATCTCCAAATPACT	631	
Dd		571	GCAATGTGAGTGCACCCTTCCTCAATACAGTTCAACTAGCCACACATCTCTAAATPACT	630	
Oy		632	CGCCATTTTAATACATTAATTAAGTAGGCAATCTGAATTAAGACACTTCACATCACAGAC	691	
Dd		631	CGCCATTTTAATACATTAATTAAGTAGGCAATCTGAATTAAGACACTTCACATCACAGAC	690	
Oy		692	CACTTTTAATATATCTAAATATCAAAAAATTAATTTTACAGATTAAGATGAAGTAATGA	751	
Dd		691	CACTTTTAATATATCTAAATATCAAAAAATTAATTTTACAGATTAAGATGAAGTAATGA	750	
Oy		752	AACGAACTATTTAGTTTTTTCACATACAAAAAAGAAATTTTGCTCGCGCGGACG	811	
Dd		751	AACGAACTATTTAGTTTTTTCACATACAAAAAAGAAATTTTGCTCGCGCGGACG	810	
Oy		812	CCAATCTCCCAATATTGGGCAACAGAGCAACAAAGAGTGCGTCCCAAGAACCAACGAC	871	
Dd		811	CCAATCTCCCAATATTGGGCAACAGAGCAACAAAGAGTGCGTCCCAAGAACCAACGAC	870	
Oy		872	AAAAAAAAAGATGATCTTAACGAGAGGACAGC	899	
Dd		871	AAAAAAAAAGATGATCTTAACGAGAGGACAGC	898	
RESULT 15					
AKI20697					
LOCUS		752 bp	mRNA	linear	
DEFINITION		Oryza sativa (japonica cultivar-group)	cDNA clone:J013170105, full insert sequence.		
ACCESSION		AKI20697.1	GI:37990320		
VERSION		AKI20697.1	GI:37990320		
KEYWORDS		FLI -cDNA; CAP trapper.			
SOURCE		Oryza sativa (japonica cultivar-group)			
ORGANISM		Oryza sativa (japonica cultivar-group)			
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
		Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;			
		Echinozoidae; Oryzae; Oryza.			
REFERENCE		1	The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yarak,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Koike,K., Namiya,T., Ohneda,E., Yahagi,W., Suzuki,K., Iiz.C., Onitsuka,K., Shisshiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group.; Otsuo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuratsaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carrinci,P., Adachi,J., Aitawa,K., Arakawa,T., Furuda,S.,		
AUTHORS					

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

2
 Adachi, J., Aizawa, K., Akinura, T., Arai, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hizemoto, N., Hirooka, T., Hori, F., Horita, I., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, T., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oseato, N., Ota, Y., Oomori, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Satazume, N., Sano, H., Saeki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shieniki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akihira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5611), 376-379 (2003)

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

3
 Kikuchi, S.
 Direct Submission
 Submitted (31-JUN-2003) Shoenji Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: kikuchi@nias.affrc.go.jp).
 Tel:81-29-838-7007, Fax:81-29-838-7007
 This clone is one of the 32k full-length cDNA clones from japonica rice.
 URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team_Kikuchi,S.,Satoch,K.,Nagata,T.,Kawagashira,N.,Doi,K.,Kishimoto,N.,Yazaki,J.,Ishikawa,M.,Yamada,H.,Ooka,H.,Hotta,I.,Kojima,K.,Namiki,T.,Ohneda,E.,Yahagi,W.,Suzuki,K.,Li,C.,Ohtsuki,K.,Shieniki,T.,Yamamoto,M.andNakahama,Y.FAIS_Genome_Sequencing_and_Analysis_Group:_Ootomo,Y.,Iida,Y.,Fujimura,T.,Ikeda,R.,Ishibiki,J.,Kawamata,M.,Kobayashi,M.,Kodama,T.,Kurosaki,T.,Kusumegi,T.,Lu,M.,Maeda,H.,Miura,J.,Mizuno,K.,Narikawa,R.,Nikura,J.,Oka,M.,Ryu,R.,Sugano,S.,Sugiyama,A.,Suzuki,Y.,Tsunoda,Y.,Ueda,M.,Xie,Q.,Yokomizo,S.,Yoshimura,A.,Matsubara,K.andMurakami,K.Genome_Exploration_Research_Group_in_Riken_Genomic_Sciences_Center_and_Genome_Science_Laboratory_in_Riken:Adachi,J.,Aizawa,K.,Akimura,T.,Arai,T.,Carninci,P.,Fukuda,S.,Hanagaki,T.,Hara,A.,Hashizume,W.,Hayashida,K.,Hayatsu,N.,Hizemoto,N.,Hirooka,T.,Hori,F.,Iida,Y.,Imamura,K.,Imotani,K.,Ishii,Y.,Ishikawa,T.,Hori,F.,Iida,Y.,Imamura,K.,Imotani,K.,Ishii,Y.,Itoh,M.,Kagawa,I.,Kanagawa,S.,Katoh,H.,Kawai,J.,Kishikawa-Hirozane,T.,Kojima,Y.,Kondo,S.,Konno,H.,Kouda,M.,Koya,S.,Kurihara,C.,Matsuyama,T.,Miyazaki,A.,Murata,M.,Nakamura,M.,Nishi,K.,Nomura,K.,Numasaki,R.,Ohno,M.,Oseato,N.,Ota,Y.,Saitoh,H.,Sakai,C.,Sakai,K.,Satazume,N.,Sano,H.,Saeki,D.,Sato,K.,Satoh,K.,Shinagawa,A.,Shiraki,T.,Sogabe,Y.,Tagami,M.,Tagami-Takeda,Y.,Tagawa,A.,Takahashi,F.,Takaku-Akihira,S.,Tanaka,T.,Tomaru,A.,Toya,T.,Waki,K.,Yasunishi,A.andHayashizaki,Y.

TITLE
JOURNAL
PUBLISHED
REFERENCE
AUTHORS

1.
 Location/Qualifiers
 1.752
 /organism="Oryza sativa (japonica cultivar-group)"

FEATURES
SOURCE

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/mol_type="mRNA"
/cultivar="Niponbare"
/db_xref="taxon:39947"
/clone="J013170105"

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ORIGIN

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Query Match      3.1%; Score 69; DB 15; Length 752;
Best Local Similarity 100.0%; Pred. No. 7.1e-24;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1023 GGAGGATCCAAAGCAAGAGGAGGACGCGACTAGAGAGAGCGGAG 1082
          |||||
Db       5    GGAGGATCCAAAGCAAGAGGAGGACGCGACTAGAGAGCGGAG 64

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QY      1083 CGACCGCCT 1091
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Db       65 CGACCGCCT 73

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Search completed: April 21, 2006, 12:06:37
 Job time : 11142 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 08:59:34 ; Search time 1221 Seconds
(without alignments)
11981.163 Million cell updates/sec

Title: US-10-541-315-1
Perfect score: 2195
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Scoring table: 0.000000
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 11
Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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11: geneseqn2003ds:*
12: geneseqn2004s:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	100.0	2195	13	AD01013 Regulator
2	1267	57.7	9361	3	Ad01285 Rice tran
C 3	1267	57.7	10639	3	Ad01286 Rice tran
4	1165	53.1	3032	13	Ad01286 FROD129-C
5	936	42.6	2191	14	Ad01286 FROD129-C
6	402	18.3	898	3	Ad01286 FROD129-C
7	402	18.3	898	3	Ad01286 FROD129-C
8	73	3.3	719	10	Ad01286 FROD129-C
9	73	3.3	724	10	Ad01286 FROD129-C
10	73	3.3	725	10	Ad01286 FROD129-C
11	73	3.3	782	10	Ad01286 FROD129-C
12	73	3.3	808	12	Ad01286 FROD129-C
13	29	1.3	48	3	Ad01286 FROD129-C
14	29	1.3	48	3	Ad01286 FROD129-C
15	27	1.2	1273	6	Ad01286 FROD129-C
16	24	1.1	24	10	Ad01286 FROD129-C
17	23	1.0	52	10	Ad01286 FROD129-C
18	23	1.0	8842	4	Ad01286 FROD129-C
19	23	1.0	8842	6	Ad01286 FROD129-C

C 20	22	1.0	22	10	Ad06857 PCR prime
C 21	22	1.0	36	3	Ad06857 PCR prime
C 22	22	1.0	36	3	Ad06857 PCR prime
C 23	22	1.0	2000	11	Ad06857 PCR prime
C 24	22	1.0	2195	13	Ad06857 PCR prime
C 25	22	1.0	6155	6	Ad06857 PCR prime
C 26	22	1.0	6233	6	Ad06857 PCR prime
C 27	22	1.0	11015	6	Ad06857 PCR prime
C 28	22	1.0	11015	6	Ad06857 PCR prime
C 29	22	1.0	11015	6	Ad06857 PCR prime
C 30	22	1.0	12269	4	Ad06857 PCR prime
C 31	22	1.0	12269	4	Ad06857 PCR prime
C 32	22	1.0	107745	13	Ad06857 PCR prime
C 33	22	1.0	256493	11	Ad06857 PCR prime
C 34	22	1.0	300000	10	Ad06857 PCR prime
C 35	22	1.0	300001	12	Ad06857 PCR prime
C 36	21	1.0	345	13	Ad06857 PCR prime
C 37	21	1.0	351	9	Ad06857 PCR prime
C 38	21	1.0	360	2	Ad06857 PCR prime
C 39	21	1.0	415	14	Ad06857 PCR prime
C 40	21	1.0	460	8	Ad06857 PCR prime
C 41	21	1.0	479	5	Ad06857 PCR prime
C 42	21	1.0	487	3	Ad06857 PCR prime
C 43	21	1.0	487	13	Ad06857 PCR prime
C 44	21	1.0	487	14	Ad06857 PCR prime
C 45	21	1.0	598	6	Ad06857 PCR prime

ALIGNMENTS

RESULT 1	AD01013	strand: DNA; 2195 BP.
ID	AD01013	
AC	AD01013	
XX	21-OCT-2004	(first entry)
DT	Regulatory DNA sequence of the rice GOS2 gene SeqID 1.	
DE	regulatory; plant; rice; GOS2; non-monocotyledonous; transgenic; ds.	
OS	Oryza sativa.	
XX	WO2004065596-A2.	
XX	05-AUG-2004.	
XX	21-JAN-2004; 2004WO-EP000645.	
XX	21-JAN-2003; 2003EP-00075207.	
XX	(CROP-) CROPPESIGN NV.	
XX	Hatzfeld Y, Inze D;	
XX	WPI, 2004-562175/54.	
XX	Use of a regulatory nucleic acid sequence for driving expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
XX	Claim 1; SEQ ID NO 1; 25pp; English.	
XX	This invention relates to a novel isolated regulatory nucleic acid sequence that is useful in the field of plant molecular biology.	
XX	Specifically, it refers to a regulatory gene of the rice GOS2 gene that can drive expression of an associated nucleic acid sequence in a non-monocotyledonous plant or plant cell.	
XX	The present invention describes introducing a regulatory sequence that results in constitutive expression (with levels similar to that of CamV 35S) of an isolated or endogenous nucleic acid sequence in a transgenic non-monocotyledonous plant. In	

CC particular, a plant cell derived from either a fodder or forage legume,
CC ornamental plant, food crop, tree or shrub, preferably, from cotton,
CC potato, tomato, cabbage, sugar beet, soybean, sunflower, or peas. This
CC polynucleotide sequence is the regulatory sequence of the rice GOS2 gene
CC of the invention.

XX Sequence 2195 BP; 639 A; 426 C; 403 G; 727 T; 0 U; 0 Other;

Query Match 100.0%; Score 2195; DB 13; Length 2195;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCGGAAAGTTTCGACCGTTTCACTCTCACTAACAATATAGGAAACGTGTGT 60
DB 1 AATCGGAAAGTTTCGACCGTTTCACTCTCACTAACAATATAGGAAACGTGTGT 60
QY 61 AATATATAAATGAGACCTTATATATATAGCGCTGATATAGAACTATAGGAAACT 120
DB 61 AATATATAAATGAGACCTTATATATATAGCGCTGATATAGAACTATAGGAAACT 120
QY 121 CATCCACCTACTTATAGTGGCAATCGGGCTAAATTAATAAGATCGCTACACTAGTTTGT 180
DB 121 CATCCACCTACTTATAGTGGCAATCGGGCTAAATTAATAAGATCGCTACACTAGTTTGT 180
QY 181 TTTCTTACTATATTAAGTGGGAAATGAATCATTTTCTTGAATATACCTTCAATC 240
DB 181 TTTCTTACTATATTAAGTGGGAAATGAATCATTTTCTTGAATATACCTTCAATC 240
QY 241 TCTGTCAATGAATTAATTAATCGAGTATGTCATTAATGTCATCAACCTCTTGAATA 300
DB 241 TCTGTCAATGAATTAATTAATCGAGTATGTCATTAATGTCATCAACCTCTTGAATA 300
QY 301 AAAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTTAAAAAAT 360
DB 301 AAAAAATCTTTCTAGCTGAACTCAATGGGTAAAGAGATATTTTTTTTTAAAAAAT 360
QY 361 AGAATGAAGATATCTGAACTGATCGGCAAGATTTAAACATATATATATATTTAT 420
DB 361 AGAATGAAGATATCTGAACTGATCGGCAAGATTTAAACATATATATATATTTAT 420
QY 421 AGTTGTGATTCGTTATATGACAGTCAATTAAGGACATGCTTACCTCATCTCAATTT 480
DB 421 AGTTGTGATTCGTTATATGACAGTCAATTAAGGACATGCTTACCTCATCTCAATTT 480
QY 481 TATTTAGTATTAAGACAAATGACTTATTTTTATTTATCTTTTTTCATAGATGC 540
DB 481 TATTTAGTATTAAGACAAATGACTTATTTTTATTTATTTATTTTCATAGATGC 540
QY 541 AAGGACTTACGACACACTTTGTGCTCATGTGATGTGTGAGTGCACCTCCTCATAC 600
DB 541 AAGGACTTACGACACACTTTGTGCTCATGTGATGTGTGAGTGCACCTCCTCATAC 600
QY 601 GTTCAACTAGGACACATCTCCAAATATCACTGCTATTTAATTAATTAAGGTACAA 660
DB 601 GTTCAACTAGGACACATCTCCAAATATCACTGCTATTTAATTAATTAAGGTACAA 660
QY 661 TCTGAATTCAGACCTTCAACATCAACACCACTTTAATTAATTAATTAATTAATTA 720
DB 661 TCTGAATTCAGACCTTCAACATCAACACCACTTTAATTAATTAATTAATTAATTA 720
QY 721 ATTAATTTTACAGAAATAGCATGAAAGTATGAAGCAACTATTTAGGTTTTTCAATCA 780
DB 721 ATTAATTTTACAGAAATAGCATGAAAGTATGAAGCAACTATTTAGGTTTTTCAATCA 780
QY 781 AAAAAAAGATTTTGTCTGTCGGCGGAGCGCAATCTCCCATATTTGGGACACAGGCA 840
DB 781 AAAAAAAGATTTTGTCTGTCGGCGGAGCGCAATCTCCCATATTTGGGACACAGGCA 840
QY 841 CAACAGATGTGCTGCCACAGAAACAACCAAAAAAGATATTAACGAGAGACACA 900
DB 841 CAACAGATGTGCTGCCACAGAAACAACCAAAAAAGATATTAACGAGAGACACA 900
QY 901 AGTCGCAACAACCTTTTAAACAGACAGGCTTTGCGGCAGAGAGAGAGGCAAG 960

DB 901 AGTCGCAACAACCTTTTAAACAGAGGCTTTGCGGCAGAGAGAGAGGCAAG 960
QY 961 AAAACCAAGCATCTCTCTCTCTCCCATCTAATTAATTTCTCCCTTTTCCCTCTATA 1020
DB 961 AAAACCAAGCATCTCTCTCTCTCCCATCTAATTAATTTCTCCCTTTTCCCTCTATA 1020
QY 1021 TAGAGGATCTCAAGCCAAAGAGAGAGACCAACCAAGACCTAGACAGACCG 1080
DB 1021 TAGAGGATCTCAAGCCAAAGAGAGAGACCAACCAAGACCTAGACAGACCG 1080
QY 1081 AGGACCGCCTTCTTCAATCCATATCTTCGGGTGAGTTCCTGGTCCATCTCCCTCC 1140
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QY 1141 TCCACCTCTCTCTCAAGAGGATATGTCCTTCGTTGTTCTTGAATTAATTTCTAGT 1200
DB 1141 TCCACCTCTCTCTCAAGAGGATATGTCCTTCGTTGTTCTTGAATTAATTTCTAGT 1200
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QY 1321 ATGGTTTCAATCTCTGAGAGCTATGGAATGAATGGTTTAAAGGATACGGAATCTT 1380
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QY 1381 GCGATTTTGTGAGTACCTTTTGTGTGAGTAAATTCAGAGACCGGTGATTTGTGCT 1440
DB 1381 GCGATTTTGTGAGTACCTTTTGTGTGAGTAAATTCAGAGACCGGTGATTTGTGCT 1440
QY 1441 GTATTAAGATCAATTTGTTGTGCTCGATTCGTGATGATGCTTCTGATTTGACGA 1500
DB 1441 GTATTAAGATCAATTTGTTGTGCTCGATTCGTGATGATGCTTCTGATTTGACGA 1500
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DB 1501 AGCTATCTCTTGTATTTATCCCATTTGAACAAAAATATCCAACTTGAACGGTCCCGT 1560
QY 1561 TGATGATTAATGAATGATGATTTCTTAAAGCTGTCCAAATTTTGGCAGCTGGTTTAA 1620
DB 1561 TGATGATTAATGAATGATGATTTCTTAAAGCTGTCCAAATTTTGGCAGCTGGTTTAA 1620
QY 1621 ATACAGTATGCCCATCAACGAATTCATGAAGAGATTAATCTTCAGAGAACGGGGAT 1680
DB 1621 ATACAGTATGCCCATCAACGAATTCATGAAGAGATTAATCTTCAGAGAACGGGGAT 1680
QY 1681 TCCCTGTTCTTCGATTTGCTTTAGTCCCAAAATTTTTTCCCAATATCTTAAAAAGT 1740
DB 1681 TCCCTGTTCTTCGATTTGCTTTAGTCCCAAAATTTTTTCCCAATATCTTAAAAAGT 1740
QY 1741 CACTTCTGCTTCAATGAATGATGTTCTAACAATATAGCTTTATAGGTTATCC 1800
DB 1741 CACTTCTGCTTCAATGAATGATGTTCTAACAATATAGCTTTATAGGTTATCC 1800
QY 1801 TAGCTGATGTTCAATGATTAATGCTTATAGTTTATGTCAGAGAGAACTTATCC 1860
DB 1801 TAGCTGATGTTCAATGATTAATGCTTATAGTTTATGTCAGAGAGAACTTATCC 1860
QY 1861 GATTTCTGATCTCCATTTTAAATTAATTAAGAAAGAACTGATGATTAAGGATTT 1920
DB 1861 GATTTCTGATCTCCATTTTAAATTAATTAAGAAAGAACTGATGATTAAGGATTT 1920
QY 1921 GGAATATTTTATTTATAGCTTCAACCCCTTCAATTTCTGAGCTGAAATCTGGCATGA 1980
DB 1921 GGAATATTTTATTTATAGCTTCAACCCCTTCAATTTCTGAGCTGAAATCTGGCATGA 1980
QY 1981 AGTCTCTCAATTTTGTTTCAATTCATGATTAATCTGATTAATCTCTGTTATC 2040

Db 1981 ACTGTCCTCAATTTGTTTCAAAATTCACATCGATTATCTATCCTTCTGTATC 2040
QY 2041 TACCTGTAGAAAGTTTCTTTTGGTTATTCCTTGACTGCTGTATACAGAAAGAAATTAT 2100
Db 2041 TACCTGTAGAAAGTTTCTTTTGGTTATTCCTTGACTGCTGTATACAGAAAGAAATTAT 2100
QY 2101 GAAGCTGTATCGGGAATAGTTATGCTGTTTCTTATGATTCATTTCTTTGTGCAATT 2160
Db 2101 GAAGCTGTATCGGGAATAGTTATGCTGTTTCTTATGATTCATTTCTTTGTGCAATT 2160
QY 2161 CTGTGTAGCTTGCACCTTTCACGCAAGAAAGTTC 2195
Db 2161 CTGTGTAGCTTGCACCTTTCACGCAAGAAAGTTC 2195
RESULT 2
AAD01285/c
ID AAD01285 standard; DNA; 9361 BP.
XX AAD01285;
XX
XX
DT 12-OCT-2000 (first entry)
XX
DE Rice transformation vector, pGOS2-hpt.
XX
XX Matrix Attachment Region; MAR; rice transformation vector; pGOS2-hpt;
KW scaffold attachment region; gene expression; transgenic organism; ds.
XX
XX Synthetic.
OS
XX WO200032800-A1.
XX
XX 08-JUN-2000.
XX
XX 30-NOV-1999; 99WO-US028123.
XX
XX 01-DEC-1998; 98US-0110437P.
XX
XX (IDWC) DOW AGROSCIENCES LLC.
XX
XX Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;
XX
XX WPI; 2000-412345/35.
XX
XX An isolated DNA molecule for use as a matrix attachment region to
PT increase expression of genes introduced in transformed plants comprises a
PT 298 base pair sequence described in the specification.
XX
XX Example 3; Page 48-51; 73pp; English.
XX
XX The patent discloses a DNA molecule, useful as matrix attachment region
CC (MAR) or scaffold attachment region, to increase the expression of genes
CC introduced in transformed plants. MARs are located in non-transcribed
CC regions of genes and form the physical boundaries of individual DNA
CC loops. They are rich in adenosine and thymine bases and contain certain
CC conserved sequence elements and structural features. They are about 300-
CC 2000 bp in length. Increased levels of expression of DNA introduced into
CC plants can be achieved by use of MAR. They can also reduce the position
CC effect in transgenic organisms. The present DNA sequence is the rice
CC transformation vector pGOS2-hpt, that contains a hygromycin selectable
CC marker driven by the 35S promoter and a GOS2/GUS nos cassette (GOS2
CC transcription initiation region/GUS structural gene/nos 3' untranslated
CC region). The GOS2 transcription initiation region in this construct is
CC comprised of 1010 bp of promoter and 170 bp of untranslated 5' leader
CC interrupted by a 1100 bp intron sequence
XX
XX
SQ Sequence 9361 BP; 2449 A; 2285 C; 2190 G; 2435 T; 0 U; 2 Other;
Query Match 57.7%; Score 1267; DB 3; Length 9361;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 623 AATATCACTGCGCTATTATACATTAGTAGCATATATCTGAATTCAGCACTTCACCA 682

Db 6472 AATATCACTGCGCTATTATACATTAGTAGCATATATCTGAATTCAGCACTTCACCA 6413
QY 683 TCACCGAGACCACTTTTAAATATATATCAAAAAATCAAAAAATTTTACAGATAGCATGA 742
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QY 743 AAGATATGAAGCAACTATTTAGTTTTCACATACAAAAAAGAAATTTTGTCTGT 802
Db 6352 AAGATATGAAGCAACTATTTAGTTTTCACATACAAAAAAGAAATTTTGTCTGT 6293
QY 803 GCGCGAGCGCCAACTCTCCCATTTTGGGACACAGGCAACACAGTGGCTCCACAGA 862
Db 6292 GCGCGAGCGCCAACTCTCCCATTTTGGGACACAGGCAACACAGTGGCTCCACAGA 6233
QY 863 ACAACCCACAAAAAAGATGATCTAACGAGGACAGCAAGTCGCGAACCACTTTTAAACA 922
Db 6232 ACAACCCACAAAAAAGATGATCTAACGAGGACAGCAAGTCGCGAACCACTTTTAAACA 6173
QY 923 GCAGGCTTTGCGCGCAGGAGAGAGAGAGAGGCAAGCAAAACCAAGCATCTCTCTCTC 982
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QY 983 CCATCTATTAATTTCTCTCCCTTTTCCCTCTCTATATAGAGGCAATCCAGCAAGAA 1042
Db 6112 CCATCTATTAATTTCTCTCCCTTTTCCCTCTCTATATAGAGGCAATCCAGCAAGAA 6053
QY 1043 GAGGAGAGACCAAGAGACAGCGCATGACAGAACCGAGCGAGCCCTTCTCATGCA 1102
Db 6052 GAGGAGAGACCAAGAGACAGCGCATGACAGAACCGAGCGAGCCCTTCTCATGCA 5993
QY 1103 TATCTTCCGATCGATTCGTGTCGATCTCTCCCTCTCACTCTCTCTCAAGGATA 1162
Db 5992 TATCTTCCGATCGATTCGTGTCGATCTCTCCCTCTCACTCTCTCTCAAGGATA 5933
QY 1163 TGTGCTTCCGATTCGTGTCGATTCGTGTCGATTCGTGTCGATTCGTGTCGATTCGT 1222
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QY 1222 TAGGAAAGGGGATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1282
Db 5872 TAGGAAAGGGGATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATG 5813
QY 1283 TTGATGTTCATGTTATCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 1342
Db 5812 TTGATGTTCATGTTATCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 5753
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Db 5752 GCTCTATGGAATGAATGTTAGGGTACGGAATCTTGCAATTTTGTGATGATCCTTTTG 5693
QY 1403 TTTGAGGTAAATACGAGACACCGGTGATTTTCTTGGTGTATTAATAATGATCTTTTG 1462
Db 5692 TTTGAGGTAAATACGAGACACCGGTGATTTTCTTGGTGTATTAATAATGATCTTTTG 5633
QY 1463 GTTCCTGATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1522
Db 5632 GTTCCTGATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5573
QY 1523 ATTGAACAATAATATCACTTTGAGAAGCGTCCGTTGATGATGATGATGATGATGATG 1582
Db 5572 ATTGAACAATAATATCACTTTGAGAAGCGTCCGTTGATGATGATGATGATGATGATG 5513
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QY 1643 ATTGAACAATAATATATCACTTTGAGAAGCGGGAATTCCTGTTCTTCGATTTGCTT 1702
Db 5452 ATTGAACAATAATATATCACTTTGAGAAGCGGGAATTCCTGTTCTTCGATTTGCTT 5393
QY 1703 TAGTCCAGAAATTTTTCCTCAAAATATCTTAAAGTCACTTCTGCTTCAAGTCAATG 1762

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Db 5332 AATTGATGCTACAAATAATGCTTTTAAATAGCGTTATCCAGCTAGTATGCTTAAATAG 5273
Qy 1823 TAAATACCCCTAATAGTTTATAGTCAGAGAGAAAGCTTATCCGATTTCTGATCTCATTTTAA 1882
Db 5272 TAAATACCCCTAATAGTTTATAGTCAGAGAGAAAGCTTATCCGATTTCTGATCTCATTTTAA 5213
Qy 1883 TTAATAGAAATGAACCTGATGAGCAATGAGCAATTCATTTGATTTTATTTTATAGCTT 1942
Db 5212 TTAATAGAAATGAACCTGATGAGCAATGAGCAATTCATTTGATTTTATTTTATAGCTT 5153
Qy 1943 TCACCCCTTCAATTTATGAGCTGAGAAAGTCTGGCATGAACTGCTCCATATTTGTTTCA 2002
Db 5152 TCACCCCTTCAATTTATGAGCTGAGAAAGTCTGGCATGAACTGCTCCATATTTGTTTCA 5093
Qy 2003 AATTCAATCGATTAATCTATGATTAATCTCTGTTATCTAATCTGTAAGAAATTTCTTTTGG 2062
Db 5092 AATTCAATCGATTAATCTATGATTAATCTCTGTTATCTAATCTGTAAGAAATTTCTTTTGG 5033
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Db 5032 GTTATTCCTTGAATCTGATTAATGAGAAAGAAATTTAATGAACTGTAATCCGGAATGTA 4973
Qy 2123 TACTGCTTGTCTTATGATTCATTTCTTTTGTGAGCTTCTTGATGCTTGCACCTTTC 2182
Db 4972 TACTGCTTGTCTTATGATTCATTTCTTTTGTGAGCTTCTTGATGCTTGCACCTTTC 4913
Qy 2183 ACCAGCAAAAGTTC 2195
Db 4912 ACCAGCAAAAGTTC 4900

RESULT 3

AAD01286/c

AAD01286 standard; DNA; 10629 BP.

XX AC AAD01286;

DT 12-OCT-2000 (first entry)

XX Rice transformation vector, pARGOS2Af-hpt.

XX Matrix Attachment Region: MAR; rice transformation vector; pARGOS2Af-hpt;

XX scaffold attachment region; gene expression; transgenic organism; ds.

XX OS Synthetic.

XX Key Location/Qualifiers

FH misc_feature 2735..3389

FT /tag= a

FT /note= "Corresponds to nucleotides 14-668 of MAR dimer-2"

FT misc_feature 7730..8384

FT /tag= b

FT /note= "Corresponds to nucleotides 1-655 of MAR dimer-1"

XX WO200032800-A1.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028123.

XX 01-DEC-1998; 98US-0110437P.

XX (DOWC) DOW AGROSCIENCES LLC.

XX Van Der Geest AHM, Ainley WM, Cowen NM, Welter ME, Woosley AT;

XX WPI; 2000-412345/35.

XX An isolated DNA molecule for use as a matrix attachment region to

PT increase expression of genes introduced in transformed plants comprises a
PT 298 base pair sequence described in the specification.

XX Example 3; Page 51-54; 73pp; English.

CC The patent discloses a DNA molecule, useful as matrix attachment region
CC (MAR) or scaffold attachment region, to increase the expression of genes
CC introduced in transformed plants. MARs are located in non-transcribed
CC regions of genes and form the physical boundaries of individual DNA
CC loops. They are rich in adenosine and thymine bases and contain certain
CC conserved sequence elements and structural features. They are about 300-
CC 2000 bp in length. Increased levels of expression of DNA introduced into
CC plants can be achieved by use of MAR. They can also reduce the position
CC effect in transgenic organisms. The present DNA sequence is the rice
CC transformation vector pARGOS2Af-hpt, identical to the vector pGOS2-hpt,
CC except that it contains a MAR dimer-2 positioned 5' to the GOS2
CC transcription initiation region and the MAR dimer-1 positioned 3' to the
CC nos 3' UTR (untranslated region). This vector is used to efficiently
CC transform monocot plants like rice

XX Sequence 10629 BP; 2904 A; 2469 C; 2369 G; 2887 T; 0 U; 0 Other;

XX Query Match 57.7%; Score 1267; DB 3; Length 10629;

XX Best Local Similarity 99.6%; Pred. No. 0; Mismatches 6; Indels 0; Gaps 0;

XX Matches 1567; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 623 AATATCACTCCCTATTTAATATATAGTATGAGCAATATCTGAATTCAGACCTTCACCA 682

Db 7111 AATATCACTCCCTATTTAATATATAGTATGAGCAATATCTGAATTCAGACCTTCACCA 7052

Qy 683 TCACCAAGACCACTTTTATATATCTAATAAATACAAATAATTTTACAAATAGCATGA 742

Db 7051 TCACCAAGACCACTTTTATATATCTAATAAATACAAATAATTTTACAAATAGCATGA 6992

Qy 743 AAAGTAAAGAAAGCAATATTAGGTTTTCATATACAAAAAAGAAATTTTGTCTGT 802

Db 6991 AAAGTAAAGAAAGCAATATTAGGTTTTCATATACAAAAAAGAAATTTTGTCTGT 6932

Qy 803 GCGGAGGCGCCATCTCCCATATTTGGGACACAGGCAACACAGAGTGGCTGCCACAGA 862

Db 6931 GCGGAGGCGCCATCTCCCATATTTGGGACACAGGCAACACAGAGTGGCTGCCACAGA 6872

Qy 863 ACAACCCCAAAAAACGATATCTTAAGGAGACAGCAAGTCCGCCAACACCTTTTAA 922

Db 6871 ACAACCCCAAAAAACGATATCTTAAGGAGACAGCAAGTCCGCCAACACCTTTTAA 6812

Qy 923 GCAGGCTTTGGGCGCAGAGAGAGAGAGAGGCAAGAAACCAAGATCTCTCTC 982

Db 6811 GCAGGCTTTGGGCGCAGAGAGAGAGAGAGGCAAGAAACCAAGATCTCTCTC 6752

Qy 983 CCATCTAATAATCTCCCTCCCTTTTCCCTCTCTATATAGAGGATCCAAAGCAAGAA 1042

Db 6751 CCATCTAATAATCTCCCTCCCTTTTCCCTCTCTATATAGAGGATCCAAAGCAAGAA 6692

Qy 1043 GAGGAGAGACCAAGAGACAGCACTAGCAAGAAAGCCGAGGACCCCTTTTGATCCA 1102

Db 6691 GAGGAGAGACCAAGAGACAGCACTAGCAAGAAAGCCGAGGACCCCTTTTGATCCA 6652

Qy 1103 TATCTCCGATCGAGTCTTGATGATCTCTTCCCTCCCACTCTCTCAAGAGGTA 1162

Db 6651 TATCTCCGATCGAGTCTTGATGATCTCTTCCCTCCCACTCTCTCAAGAGGTA 6572

Qy 1163 TGTGCCCTTCGATGTTCTTGATTTATGTTCTTAAAGTTGTATGATCGGGCGTTGATGT 1222

Db 6571 TGTGCCCTTCGATGTTCTTGATTTATGTTCTTAAAGTTGTATGATCGGGCGTTGATGT 6512

Qy 1223 TAGAAAGGGGATCTGATCTGATGATTTCTGTTCTTGATTTGGATAGAGGGTTC 1282

Db 6511 TAGAAAGGGGATCTGATCTGATGATTTCTGTTCTTGATTTGGATAGAGGGTTC 6452

Qy 1283 TTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1342

Db 6451 TTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6392

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QY 1343 GCTATGAGAAATGATGTTAGGATCGAATCTTGCAATTTTGTGAGTACCTTTTG 1402
DB 6391 GCTCTATGAGAAATGATGTTAGGATCGAATCTTGCAATTTTGTGAGTACCTTTTG 6332
QY 1403 TTTGAGATGAAATCAAGACCCGGTATTTGCTGTGTGTAATAAAGTACATTTGTTTG 1462
DB 6331 TTTGAGATGAAATCAAGACCCGGTATTTGCTGTGTGTAATAAAGTACATTTGTTTG 6272
QY 1463 GTCCCTGATTTCTGTAGTATGCTTCTGATTTGAGCAAGCTATCTTGTGTTATTCCTT 1522
DB 6271 GTCCCTGATTTCTGTAGTATGCTTCTGATTTGAGCAAGCTATCTTGTGTTATTCCTT 6212
QY 1523 ATTGAACAAAAATATCAACTTTGAAAGCGTCCCGTTGATGATGATGATGATGAT 1582
DB 6211 ATTGAACAAAAATATCAACTTTGAAAGCGTCCCGTTGATGATGATGATGATGATGAT 6152
QY 1583 CTTAAGCCTGTCCAAAATTTCCGACGCTGCTGTTTAAATACATGATGATGATGATGAT 1642
DB 6151 CTTAAGCCTGTCCAAAATTTCCGACGCTGCTGTTTAAATACATGATGATGATGATGAT 6092
QY 1643 ATTCATGAAACAGTATATATCTCTGAGAACAGGGGATCCCTGTTCCGATTTGCTT 1702
DB 6091 ATTCATGAAACAGTATATATCTCTGAGAACAGGGGATCCCTGTTCCGATTTGCTT 6032
QY 1703 TAGTCCCAAGATTTTTCCTCCAAATATCTTAAAGTACATTTCTGTGATTCAGTTCAAG 1762
DB 6031 TAGTCCCAAGATTTTTCCTCCAAATATCTTAAAGTACATTTCTGTGATTCAGTTCAAG 5972
QY 1763 AATTGATGCTACAAATATGCTTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 1822
DB 5971 AATTGATGCTACAAATATGCTTTTAAAGCTTAAAGCTTAAAGCTTAAAGCTTAAAG 5912
QY 1823 TAATACCCCTATAGTTAGTACGAGAGAAAGTATCCGATTCGATCCGATTTTAA 1882
DB 5911 TAATACCCCTATAGTTAGTACGAGAGAAAGTATCCGATTCGATCCGATTTTAA 5852
QY 1883 TTATATGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1942
DB 5851 TTATATGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5792
QY 1943 TCACCCCTCATTTATCTGAGCTGAAAGTCTGAGCAATGCTGCTCAATTTGTTTCA 2002
DB 5791 TCACCCCTCATTTATCTGAGCTGAAAGTCTGAGCAATGCTGCTCAATTTGTTTCA 5732
QY 2003 AATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2062
DB 5731 AATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5672
QY 2063 GTTATTCCTGACTGCTGATTAAGAAAGAAATTTATGAAAGCTGATTCGGATAGTTA 2122
DB 5671 GTTATTCCTGACTGCTGATTAAGAAAGAAATTTATGAAAGCTGATTCGGATAGTTA 5612
QY 2123 TACTGCTGTTCTTATGATTCATTTCTTGTGCACTGCTGTTGTTGCACTTTC 2182
DB 5611 TACTGCTGTTCTTATGATTCATTTCTTGTGCACTGCTGTTGTTGCACTTTC 5552
QY 2183 ACCAGCAAGTTC 2195
DB 5551 ACCAGCAAGTTC 5539
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RESULT 4
ADT92083
ID ADT92083 standard; DNA; 3032 BP.

AC ADT92083;

DT 13-JAN-2005 (first entry)

DE PRO0129-CD51585 expression cassette for MT2a.

XX MT2a; plant growth; plant development; transgenic; genetic modification;

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KW metallochionein; metal accumulation; abiotic stress; growth regulator;  
KW gene; ss.  
XX  
OS Synthetic.  
XX  
PN MO2004090142-A2.  
XX  
PD 21-OCT-2004.  
XX  
PF 14-APR-2004; 2004WO-EP050519.  
XX  
PR 14-APR-2003; 2003EP-00076086.  
XX  
PA (CROP-) CROPDSEIGN NV.  
PI Sanz Molinero AI;  
XX  
DR WPI; 2004-748770/73.  
XX  
PT Modifying plant growth and development for altering growth  
PT characteristics in plants, comprises introducing a genetic modification  
PT in the plant and selecting modulated expression of a nucleic acid  
PT encoding a metallochionein protein.  
XX  
PS Claim 13; SEQ ID NO 7; 49pp; English.  
XX  
CC The invention relates to modifying plant growth and development and  
CC involves introducing a genetic modification in the plant and selecting  
CC for modulated expression in the plant of a nucleic acid encoding a  
CC metallochionein protein, provided that the modified growth and  
CC development is not increased metal accumulation or increased tolerance or  
CC resistance to abiotic stress. In modifying plant growth and development,  
CC the modified plant growth and development is increased yield, preferably  
CC an increase of biomass and/or seed yield, when compared to corresponding  
CC wild type plants. Genetic modification comprises introducing an isolated  
CC nucleic acid encoding a metallochionein protein into a plant. The nucleic  
CC acid encoding a metallochionein protein encodes a type 2 metallochionein  
CC and is derived from a plant, preferably a dicotyledonous plant, more  
CC preferably from the family Brassicaceae, e.g. Arabidopsis thaliana. The  
CC expression of the nucleic acid encoding a metallochionein is driven by a  
CC constitutive promoter, preferably the rice GOS2 promoter. The  
CC metallochionein protein and its homologues, derivatives, and active  
CC fragments, and the encoding polynucleotides are useful for modifying the  
CC growth characteristics of plants, provided that the modified growth and  
CC development is not increased metal accumulation or increased tolerance or  
CC resistance to abiotic stress. They are also useful as a growth regulator.  
CC The method is useful for modifying plant growth and development. It is  
CC also useful for producing plants with altered growth characteristics,  
CC e.g. increased yield, increased biomass, increased total above ground  
CC area, increased plant height, increased number of tillers, increased  
CC number of primary panicles, increased total number of seeds, or increased  
CC harvest index. The present sequence represents the nucleotide sequence of  
CC an PRO0129-CD51585 -zein and rps double terminator expression  
CC cassette for the expression of A. thaliana AtMT2a gene.  
XX  
SQ Sequence 3032 BP; 917 A; 595 C; 581 G; 939 T; 0 U; 0 Other;
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Query Match 53.1%; Score 1165; DB 13; Length 3032;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 623 AATATCACTCGCTATTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 682  
DB 621 AATATCACTCGCTATTTATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680  
QY 683 TCACCAAGACCTTTTATATATATCTTAAATCAAAAAATATTTTACGATATGATCA 742  
DB 681 TCACCAAGACCTTTTATATATATCTTAAATCAAAAAATATTTTACGATATGATCA 740  
QY 743 AAGATATGAAAGCAACTATTTAGTTTTCATATCAAAAAAAGATTTGCTGCT 802  
DB 741 AAGATATGAAAGCAACTATTTAGTTTTCATATCAAAAAAAGATTTGCTGCT 800
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QY	803	ACGCGAGGCGCAATCTCCATATTTGGGACACAGGCAACAACAGATGGCTGGCCACAGA	862
Db	801	GCGCAGGCGCAATCTCCATATTTGGGACACAGGCAACAACAGATGGCTGGCCACAGA	860
QY	863	ACAACCCACAATAAAACGATGATCTTAACGAGAGACAGCAAGTCCGCACAACTTTTAACA	922
Db	861	ACAACCCACAATAAAACGATGATCTTAACGAGAGACAGCAAGTCCGCACAACTTTTAACA	920
QY	923	GCAGGCTTTGCGGCCAGGAGAGAGAGAGAGGCAAGAAAAACAAAGATCTCTCTCTC	982
Db	921	GCAGGCTTTGCGGCCAGGAGAGAGAGAGAGGCAAGAAAAACAAAGATCTCTCTCTC	980
QY	983	CCATCTATTAATTTCTCTCCCTCTTTTCCCTCTCTATATPAGAGGCAATCCAAAGCAAGAA	1042
Db	981	CCATCTATTAATTTCTCTCCCTCTTTTCCCTCTCTATATPAGAGGCAATCCAAAGCAAGAA	1040
QY	1043	GAGGAGAGACACCAAGGACACGCGACTAGCAGAAACCGACGACCGGCTTTCTTGATCCA	1102
Db	1041	GAGGAGAGACACCAAGGACACGCGACTAGCAGAAACCGACGACCGGCTTTCTTGATCCA	1100
QY	1103	TATCTTCCGATCGAGTTCTTGGTCGATCTTCCCTCTCCACCTCTCTCACAGGGTA	1162
Db	1101	TATCTTCCGATCGAGTTCTTGGTCGATCTTCCCTCTCCACCTCTCTCACAGGGTA	1160
QY	1163	TGTGCGCTTCGGTGTCTTGGAATTAATGTTCTTAGGTGTGTGTAGTACGGCGTTGATGT	1222
Db	1161	TGTGCGCTTCGGTGTCTTGGAATTAATGTTCTTAGGTGTGTGTAGTACGGCGTTGATGT	1220
QY	1223	TAGGAAAGGGGATCTGTATCTGTGTGATTCCTGTCTTGATTTGGGATAGAGGGGTTT	1282
Db	1221	TAGGAAAGGGGATCTGTATCTGTGTGATTCCTGTCTTGATTTGGGATAGAGGGGTTT	1280
QY	1283	TTGATGTTGCATGTTATCGGTTCCGTTTGATTAAGTATGATGTTTCAATGCTGTGAGA	1342
Db	1281	TTGATGTTGCATGTTATCGGTTCCGTTTGATTAAGTATGATGTTTCAATGCTGTGAGA	1340
QY	1343	GCTCTATGGAATAAGATGTTTAGGGATCGGAATCTTGCGATTTGTGATACCTTTTG	1402
Db	1341	GCTCTATGGAATAAGATGTTTAGGGATCGGAATCTTGCGATTTGTGATACCTTTTG	1400
QY	1403	TTTGAAGTAAATCGAGACACCGGATTTTGCTGTGGTATPATAAGTACATTTGTTTG	1462
Db	1401	TTTGAAGTAAATCGAGACACCGGATTTTGCTGTGGTATPATAAGTACAGTGTGTTG	1460
QY	1463	GTCTCGATTCGTGATGATGCTTCTCGATTTGACGAAGCTATCTTTGTTATTCCT	1522
Db	1461	GTCTCGATTCGTGATGATGCTTCTCGATTTGACGAAGCTATCTTTGTTATTCCT	1520
QY	1523	ATTGAACAAATAATTCACCTTTGAGAAGCGGTCCGTTGATGAGATTGAATGATGTT	1582
Db	1521	ATTGAACAAATAATTCACCTTTGAGAAGCGGTCCGTTGATGAGATTGAATGATGATGTT	1580
QY	1583	CTTAAGCCTGTCCAAAATTTGGAGCTGGCTGTTTAAATACAGTAGCCCATCAAGAA	1642
Db	1581	CTTAAGCCTGTCCAAAATTTGGAGCTGGCTGTTTAAATACAGTAGCCCATCAAGAA	1640
QY	1643	ATTCAATGAAAACAGTTAATCTCTCAGAGAACAGGGGATTCCTGTGTTCTCCGATTTGCTT	1702
Db	1641	ATTCAATGAAAACAGTTAATCTCTCAGAGAACAGGGGATTCCTGTGTTCTCCGATTTGCTT	1700
QY	1703	TAGTCCAGAAATTTTTTCCCAATATCTTAAAAAGTCACTTTCGTGTTCAGTTCAATG	1762
Db	1701	TAGTCCAGAAATTTTTTCCCAATATCTTAAAAAGTCACTTTCGTGTTCAGTTCAATG	1760
QY	1763	AATTGATTGCTACAAATATATGTTTAAAGGTTATCCTACTGTGATGAGTTTAATAGG	1822
Db	1761	AATTGATTGCTACAAATATATGTTTAAAGGTTATCCTACTGTGATGAGTTTAATAGG	1820
QY	1823	TAAATACCCCTATAGTTTATAGTCAGAGAGAACTTATCCGATTTCTGATCTCATTTTAA	1882
Db	1821	TAAATACCCCTATAGTTTATAGTCAGAGAGAACTTATCCGATTTCTGATCTCATTTTAA	1880
QY	1883	TTAATATGAATGAATCTGTAGCATAGCAGTATTCATTTGATTAATTTTTTATTAAGCTT	1942

Db	1881	TTATATGAAATGAACTGTAGCATAGACGATTCATTGGATTATTTTTTTATATAGCTC	1940
Qy	1943	TCACCCCTTCATTATTCGTAGCTGAAAAGTCGCGATGACTGCTCAATTTGTGTTTCA	2002
Db	1941	TCACCCCTTCATTATTCGTAGCTGAAAAGTCGCGATGACTGCTCAATTTGTGTTTCA	2000
Qy	2003	AATTCACATCGATATCGATCGATTTATCCCTGTCATCGACCTGAGAAAGTTCTTTTTG	2062
Db	2001	AATTCACATCGATATTCATGACATTTATCTCTTGATCTACCTGTAGAAAGTTCTTTTTG	2060
Qy	2063	GTATATTCCTTGACTGCTGTGATTACAGAAAGAAATTTATGAACTGTATCGGATAGTGA	2122
Db	2061	GTATATTCCTTGACTGCTGTGATTACAGAAAGAAATTTATGAACTGTATCGGATAGTGA	2120
Qy	2123	TACTGCTTGTTCTTATGATTCATTTCTTTGTGCAAGTTCTTGCTGTAAGCTTGCCACTTTC	2182
Db	2121	TACTGCTTGTTCTTATGATTCATTTCTTTGTGCAAGTTCTTGCTGTAAGCTTGCCACTTTC	2180
Qy	2183	ACGAGCAAAAGTTC	2195
Db	2181	ACGAGCAAAAGTTC	2193

RESULT 5	
ADY69039	
ID	ADY69039 standard; DNA; 2191 BP.
XX	
AC	ADY69039;
XX	
DT	02-JUN-2005 (first entry)
XX	
DE	GOS2 promoter DNA.
XX	
KW	plant; crop improvement; B-type cyclin dependent kinase; CDK; ds;
KW	promoter; GOS2.
XX	
OS	unidentified.
XX	
PN	WO2005024029-A2.
XX	
PD	17-MAR-2005.
XX	
PF	03-SEP-2004; 2004WO-EP052035.
XX	
PR	05-SEP-2003; 2003EP-00077811.
XX	
PA	(CROP-) CROPDESIGN NV.
XX	
P1	Broekaert W, Frankard V, Hatzfeld Y, Mironov V;
XX	
DR	WPI; 2005-223384/23.
XX	
PT	Improving plant growth characteristics, e.g. increased yield, increased
PT	growth rate, or modified architecture, comprises increasing expression,
PT	activity and/or levels in a plant of B-type cyclin dependent Kinase.
XX	
PS	Disclosure; SEQ ID NO 15; 79bp; English.
XX	
CC	Improving plant growth characteristics, e.g. increased yield, increased
CC	growth rate, or modified architecture, comprises increasing expression in
CC	a plant of a nucleic acid encoding a B-type cyclin dependent Kinase (CDK)
CC	protein and/or increasing activity and/or levels in a plant of a B-type
CC	CDK protein. INDEPENDENT CLAIMS are also included for: Plants obtained
CC	using the method above; construct comprising (i) a B-type CDK
CC	gene/nucleic acid encoding a B-type CDK protein, or (ii) a nucleic acid
CC	encoding a CDK mutant, which CDK mutant comprises at least one of the 7
CC	amino acid position changes or at least one of the 8 amino acid position
CC	changes listed in the disclosure, (iii) one or more control sequences
CC	capable of driving expression of the nucleic acid of (i) or (ii), and
CC	optionally (iv) a transcription termination sequence; a method for
CC	producing transgenic plant having improved growth characteristics, e.g.
CC	increased yield, increased growth rate, or modified architecture, which

growth characteristics are improved relative to growth characteristics of corresponding wild type plants; transgenic plant having improved growth characteristics, e.g. increased yield, increased growth rate, or modified architecture, the plant has increased expression of a B-type CDK nucleic acid and/or increased activity and/or levels in a plant of a B-type CDK protein relative to corresponding wild type plants; a composition comprising a protein comprising a sequence of 309, 311, or 315 amino acids (EVEN SEQ ID NOS: 2-6), or its homologue, derivative, or active fragment, used as a growth regulator; a screening method for identifying mutant plant CDKs having enhanced CDK activity relative to corresponding non-mutated plant CDKs; a screening method for identifying substantially non-active plant CDKs, but are capable of binding to plant ICKs; mutant CDKs obtained using the methods of (6) and (7), where the mutants bind to cyclin but not to ICK as listed in the disclosure, or where the mutants bind to ICK but not to cyclin as listed in the disclosure; an isolated nucleic acid molecule comprising (i) a nucleic acid encoding a CDK mutant comprising any of the 5 sequences of 294 amino acids each (SEQ ID NOS: 9-13) or (ii) a nucleic acid molecule encoding a homologue, derivative or active fragment of a CDK mutant of SEQ ID NOS: 9-11, where the homologue, derivative or active fragment comprised at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, (iii) a nucleic acid capable of hybridizing with a nucleic acid of (i) or (ii), where the hybridizing sequence encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, (iv) a nucleic of (i) to (iii) which is degenerate as a result of the genetic code, (v) allelic variants of (i) to (iv), where the allelic variant encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure, or (vi) alternative splice variants of nucleic acids of (i) to (v), where the alternative splice variants encodes an amino acid comprising at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure; and a CDK mutant comprising (i) an amino acid sequence of SEQ ID NOS: 9-13, or (ii) a fragment of SEQ ID NOS: 9-13 where the fragment comprises at least one of the 7 amino acid position changes or at least one of the 8 amino acid position changes listed in the disclosure. Preferred Method: Increasing expression is effected by introducing and expressing in a plant a B-type CDK nucleic acid. The B-type CDK is derived from a plant, algal, or fungal source. The B-type CDK derived from a plant is from a dicotyledonous plant, preferably from the family Brassicaceae, specifically Arabidopsis thaliana. The B-type CDK is a class I B-type CDK, preferably a CDK B1,1 or CDK B1,2 from A. thaliana. The B-type CDK is a class 2 B-type CDK, preferably a CDK B2,2 from A. thaliana. The CDK B1,1 nucleic acid comprises a sequence of 930 bp (SEQ ID NO: 1), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 1, and where the CDK B1,1 protein comprises a sequence of 980 bp (SEQ ID NO: 2) or its homologue, derivative or active fragment. The CDK B1,2 nucleic acid comprises a sequence of 936 bp (SEQ ID NO: 3), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 3, and where the CDK B1,2 protein comprises a sequence of SEQ ID NO: 4 or its homologue, derivative or active fragment. The CDK B2,2 nucleic acid comprises a sequence of 948 bp (SEQ ID NO: 5), or its portion, or a nucleic acid capable of hybridizing to SEQ ID NO: 5, and where the CDK B2,2 protein comprises a sequence of SEQ ID NO: 6 or its homologue, derivative or active fragment. The B-type CDK is a variant nucleic acid or variant amino acid, e.g. functional portions of, sequences capable of hybridizing to, alternative splice variants of, or allelic variants of a B-type CDK nucleic acid/gene, homologues, derivatives, or active fragments of a B-type CDK protein, or mutant B-type CDKs. The expression of the CDK B1,1 nucleic acid is driven by a promoter active in young, expanding tissue, preferably where the promoter is beta expansin promoter. The expression of CDK B1,2 nucleic acid CDK B2,2 nucleic acid is driven by a constitutive promoter, specifically a GOS 2 promoter. The increased yield comprises increase in area, increase in the number of panicles, increased in height, increase in the number of seeds, increase in the number of filled seed, increase in total weight of seeds, increase in thousand kernel weight (TKW), or an increase in harvest index, each relative to control plants. The modified architecture includes increase in aboveground are, increase in the number of panicles or increase in height. Producing transgenic plant having improved characteristics, e.g. increased yield, increased growth rate, or modified architecture, e.g. growth characteristics are

CC improve relative to growth characteristics of corresponding wild type
CC plants, comprises introducing into a plant or a plant cell a B-type CDK
CC gene/nucleic, or a nucleic acid encoding a CDK mutant comprising at least
CC one of the 7 amino acid position changes listed in the disclosure, and
CC cultivating the plant cell under conditions promoting regeneration and
CC mature plant growth. Identifying mutant plant CDKs having enhanced CDK
CC activity relative to corresponding non-mutated plant CDKs comprises
CC providing plant-derived CDK mutants, identifying cyclin dependent kinase
CC inhibitor (ICK) non reacting mutants, identifying mutants having cyclin-
CC binding activity, and optionally a yeast complementation assay on
CC resultant mutants. Identifying substantially non-active plant CDKs, but
CC are capable of binding to plant ICKs, comprises providing plant-derived
CC CDK mutants, identifying plant-derived ICK binding mutants, and
CC identifying non-cyclin binding mutants. The CDK mutants are provided by
CC providing a wild type plant CDK and mutating the CDK at least 1 amino
CC acid position. Preferred Transgenic Plant: The plant is a
CC monocotyledonous plant. The CDK B-type nucleic or CDK B-type amino acid
CC is useful for improving the growth characteristics of a plant, the growth
CC characteristics is increased yield, increased growth rate, or modified
CC architecture (claimed).

SQ Sequence 2191 BP; 638 A; 431 C; 403 G; 719 T; 0 U; 0 Other;

Query Match	42.6%	Score 936	DB 14	Length 2191
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Matches 1306; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

623 AATATCACTGGCTATTTAATACATTAGGTAGCAATATCTGAATTCAAGCACTTCACCA 682

Db 621 AATATCACTCGCCTATTTAATACATTTAGGTAGCAATATCTGAATTCAAGCACTCCACCA 680

683 TCACCAGACCACTTTTAATAATATCTAAATACAAAAATAATTTTACAGATAGCATGA 742

Db 681 TCACCAGACCACTTTAATAATATCTAAATACAAAAATAATTTTACAGATAGCATTGA 740

743 AAGTATGAACGACTATTAGGTTTTCACATACAAAAAAGAATTTTCCTCGT 802

DB 741 AAGTATGAAACGAACATATAGGTCTTTCACATACAAAAAAGAATTTGCTCGT 800

803 GCGCAGCGCCAAICICCCAAIIGCGCACACAGCGAACACACAGAGIAGCIGCCACACAGAA 002

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2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 104

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1041 GAGGAGAGCAACCAAGGACACCGCACTTAGCAGAGACCGAGCAACCGCTTCTTCGATCCA 1100

1103 TATCTTCGGTCGAGTTCCTGGTCGATCTCTTCCCTCCACCTCCTCCTCCTACAGGTA 1162

Db 1101 TATCTCCGGTCGAGTCTTGGTCGATCTTCCCTCCACCTCCTCCTCACAGGTA 1160

1163 TGTGCCCTTCGGTGTCTCTTGATTTATTGTTCTAGGTTGTGTAGTACGGGCGTTGATGT 1222

Db 1161 TGTGCCCTTCGGTGTCTTGGATTATTGTTCTAGGTGTGTAGTACGGCGTTGATGT 1220

1223 TAGGAAGGGATCTGTATCTGTGATGATTCTCTGTTCTTGGAATTGGGATAGAGGGTTC 1282

Db 1221 TAGGAAGGGATCTGTATCTGTGATGATTCTCTGTTCTTGGATTGGGATAGAGGGGTTCT 1280

1283 TTGATGTTGCATGTTATCGGTTCCGTTTGATTAGTAGTATGGTTTTCATCGTCTGAGA 1342

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DB 751 AACGAATATTGTTGGTTCATCTACAAAAAAGATTTTGTCTGTGGCGAGCG 810
QY 812 CCAATCTCCATTTGGGACACAGGCAACAGAGTGGTCCCAACAGAACCCAC 871
DB 811 CCAATCTCCATTTGGGACACAGGCAACAGAGTGGTCCCAACAGAACCCAC 870
QY 872 AAAAAAGATGATCTAAGGAGACAGC 899
DB 871 AAAAAAGATGATCTAAGGAGACAGC 898
RESULT 7
AAC87195
ID AAC87195 standard; DNA; 898 BP.
XX
AC AAC87195;
XX
DT 09-MAR-2001 (first entry)
XX
DE Rice GOS2 promoter enhancer element, SEQ ID NO:50.
XX
KM Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;
KW glyphosate resistance; herbicide resistance; transgenic plant;
expression construct; enhancer element; da.
XX
OS Oryza sativa.
XX
PN MO200066748-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000MO-GB001573.
XX
PR 29-APR-1999; 99GB-00009968.
PR 29-JUL-1999; 99GB-00017834.
PR 29-JUL-1999; 99GB-00017839.
PR 29-JUL-1999; 99GB-00017840.
PR 29-JUL-1999; 99GB-00017846.
PR 29-JUL-1999; 99GB-00017847.
PR 21-DEC-1999; 99GB-00030200.
PR 21-DEC-1999; 99GB-00030204.
PR 21-DEC-1999; 99GB-00030207.
PR 21-DEC-1999; 99GB-00030209.
PR 21-DEC-1999; 99GB-00030213.
XX
PA (ZENB) ZENECA LTD.
XX
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;
XX
DR WPI; 2000-687544/67.
XX
PT Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase,
PT having resistance or tolerance to glyphosate herbicide.
XX
PS Claim 18; Page 56; 87pp; English.
XX
CC The invention relates to rice 5-enolpyruvylshikimate phosphate synthase
CC (EPSPS) genomic DNA (AAC87188). The invention also relates to an
CC expression cassette comprising, in the 5'-3' direction, one or more
CC transcripional enhancer elements selected from AAC87190-GB7196), the
CC rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast
CC transit peptide, genomic DNA encoding a EPSPS protein modified such that
CC it is resistant to glyphosate (AAC87189), and a transcriptional
CC terminator. The glyphosate resistant EPSPS contains a region (AAB29793)
CC containing two amino acid substitutions relative to the corresponding
CC wild-type region (AAB29792). The invention also encompasses plant genomic
CC EPSPS sequences identified via screening with a rice EPSPS intronic
CC sequence, vectors and host plant cells comprising a nucleic acid sequence
CC of the invention; transgenic plants (and tissues and seeds thereof)
CC comprising a nucleic acid sequence of the invention, optionally further
CC transformed with a DNA encoding an insect, fungal, viral, bacterial,

CC nematode, stress or herbicide resistance protein; and methods of
CC producing the transgenic plants of the invention. The nucleic acids and
CC constructs of the invention are used to produce a wide variety of
CC morphologically normal, glyphosate resistant plants. The glyphosate
CC resistant plants produced are particularly maize, soybean, cotton,
CC sugarcane and canola, but also other field crops, fruits and vegetables,
CC turf and forage grasses and nut-producing plants. The plants are
CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,
CC stress, desiccation and/or other herbicides. They can be used in the
CC production of a herbicidal target for the high throughput in vitro
CC screening of potential herbicides. The present sequence represents an
CC enhancer element which may be used in the rice EPSPS expression cassette
CC of the invention
XX
SQ Sequence 898 BP; 320 A; 166 C; 137 G; 275 T; 0 U; 0 Other;
Query Match 18.3%; Score 402; DB 3; Length 898;
Best Local Similarity 99.3%; Pred. No. 2, 1e-176;
Matches 862; Conservative 0; Mismatches 2; Indels 4; Gaps 2;
QY 33 CTAACTAACATATAGGAAAGCTGCTAAATATTAATGAGACCTTATATATGAGCCG 92
DB 34 CTAACTAACATATAGGAAAGCTGCTAAATATTAATGAGACCTTATATATGAGCCG 93
QY 93 TGATTAAGTAACTATGTAAGAAAACTCATCCACTTATAGTGGCAATGGGCTAA 152
DB 94 TGATTAAGTAACTATGTAAGAAAACTCATCCACTTATAGTGGCAATGGGCTAA 153
QY 153 TAAAAAGAGTGGCTAACTAGTTTCTTCTTAAATTAAGGGAATAATGAATC 212
DB 154 TAAAAAGAGTGGCTAACTAGTTTCTTCTTAAATTAAGGGAATAATGAATC 213
QY 213 ATTATGCTTAAGATATAGCTTCACTCTCTGATGAAGTTAAATTTATCGAGTAGCC 272
DB 214 ATTATGCTTAAGATATAGCTTCACTCTCTGATGAAGTTAAATTTATCGAGTAGCC 273
QY 273 ATAAATGTCATCAAACTCTCTTGAATAAAAATCTTCTAGCTGAATCAATGGCTAA 332
DB 274 ATAAATGTCATCAAACTCTCTTGAATAAAAATCTTCTAGCTGAATCAATGGCTAA 333
QY 333 AAGAGATATTTTTTTTAAAAAATGAATGAAGATTTCTGAACCTATCGCAAG 392
DB 334 AAGAGATATTTTTTTTAAAAAATGAATGAAGATTTCTGAACCTATCGCAAG 390
QY 393 ATTAAACAT 452
DB 391 ATTAAACAT 450
QY 453 AGGACATGCTTACTCATCTCAATTTTATATATATATATATATATATATATATAT 512
DB 451 AGGACATGCTTACTCATCTCAATTTTATATATATATATATATATATATATATAT 510
QY 513 TAT 572
DB 511 TAT 570
QY 573 GGATGATGATGAGCACTCTC-ATACAGTTCACACTAGGACACATCTCATATCACT 631
DB 571 GGATGATGATGAGCACTCTC-ATACAGTTCACACTAGGACACATCTCATATCACT 630
QY 632 CGCTAT 691
DB 631 CGCTAT 690
QY 692 CACTTTAT 751
DB 691 CACTTTAT 750
QY 752 AAGGAAT 811
DB 751 AAGGAAT 810
QY 812 CCAATCTCCATTTGGGACACAGGCAACAGAGTGGTCCCAAGAACCCAC 871

RESULT 12
ADJ39051
ID ADJ39051 standard; cDNA; 808 BP.
XX
XX
AC ADJ39051;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plant cDNA #51.
XX
KM Plant; gene; ss; transfection; plant genome augmentation; cereal;
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.
XX
OS Bkaryota.
XX
PN US2004016025-A1.
XX
PD 22-JAN-2004.
XX
XX 26-SEP-2002; 2002US-00260238.
PF
PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.
XX
PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J.
PA (GORE/) GORE S A.
PA (KATA/) KATAGIRI F.
PA (KEPS/) KEPS J.
PA (PROV/) PROVART N.
PA (RICK/) RIQUE D.
PA (ZHUT/) ZHU T.
XX
PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Provart N, Rique D, Zhu T;
XX
DR WPI; 2004-190374/18.
XX
PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.
XX
PS Claim 68; SEQ ID NO 51; 230bp; English.
XX
CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 808 BP; 203 A; 198 C; 188 G; 219 T; 0 U; 0 Other;

Query Match 3.3%; Score 73; DB 12; Length 808;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2122 ATACGCTTGTTCTTATGATTCATTCTTGTGAGTCTTGATGCTTGCCACTT 2181
DB 139 ATACTGCTTGTTCTTATGATTCATTCTTGTGAGTCTTGATGCTTGCCACTT 198

QY 2182 CACCAGCAAGTT 2194
DB 199 CACCAGCAAGTT 211

RESULT 13
AAC8379
ID AAC8379 standard; DNA; 48 BP.
XX
AC AAC8379;
XX
DT 02-MAR-2001 (first entry)
XX
DE Primer GOS5.
XX
KM Glyphosate; 5-enolpyruvylshikimate phosphate synthase; EPSPS;
KM herbicide resistance; ss.
XX
OS Synthetic.
XX
PN WO20006746-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000WO-GB0015559.
XX

PR 29-APR-1999; 99GB-00009971.
PR 29-APR-1999; 99GB-00009972.
PR 29-JUL-1999; 99GB-00017837.
PR 29-JUL-1999; 99GB-00017842.
PR 21-DEC-1999; 99GB-00030190.
PR 21-DEC-1999; 99GB-00030206.
PR 21-DEC-1999; 99GB-00030214.
PR 21-DEC-1999; 99GB-00030216.
XX
PA (ZENB) ZENNECA LTD.
XX
PI Hawkes TR, Warner SAJ, Andrews CJ, Bachoo S, Pickerill AP;
XX
DR WPI; 2000-679763/66.
XX
PT Novel polynucleotide encoding the rice 5-enolpyruvylshikimate phosphate
PT synthase, used to produce glyphosate tolerant or resistant plants.
XX
PS Example 4; Page 15; 85pp; English.
XX
CC The present invention relates to a glyphosate resistant rice 5-
CC enolpyruvylshikimate phosphate synthase (EPSPS) gene. This gene can be
CC used to produce plant tissue and/or morphologically normal fertile whole
CC plants which are tolerant or resistant to glyphosate herbicide, and in
CC the production of a herbicidal target for the high throughput in vitro
CC screening of potential herbicides
XX
SQ Sequence 48 BP; 10 A; 16 C; 11 G; 11 T; 0 U; 0 Other;

Query Match 1.3%; Score 29; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCGAAGTTCTTGACCGTTTTCAC 29
DB 19 AATCGAAGTTCTTGACCGTTTTCAC 47

RESULT 14
AAC87162 standard; DNA; 48 BP.
XX
AC AAC87162;
XX
DT 09-MAR-2001 (first entry)
XX
DE Rice G052 enhancer element PCR primer, SEQ ID NO:17.
XX
KM Rice EPSPS; 5-enolpyruvylshikimate phosphate synthase;
KM glyphosate resistance; herbicide resistance; transgenic plant;
KM expression construct; enhancer element; PCR primer; ss.
XX
OS Oryza sativa.
XX
PN WO200066748-A1.
XX
PD 09-NOV-2000.
XX
PF 20-APR-2000; 2000MO-GB001573.
XX
PR 29-APR-1999; 99GB-00009968.
XX 29-JUL-1999; 99GB-00017834.
PR 29-JUL-1999; 99GB-00017839.
XX 29-JUL-1999; 99GB-00017840.
PR 29-JUL-1999; 99GB-00017845.
XX 29-JUL-1999; 99GB-00017847.
PR 21-DEC-1999; 99GB-00030200.
XX 21-DEC-1999; 99GB-00030204.
PR 21-DEC-1999; 99GB-00030207.
XX 21-DEC-1999; 99GB-00030209.
PR 21-DEC-1999; 99GB-00030213.
XX
PA (ZENEC) ZENECA LTD.
XX
PI Hawkes TR, Warner SMJ, Andrews CJ, Bachoo S, Pickering AP;
XX
XX WPI; 2000-687544/67.
XX
PT Novel polynucleotide encoding 5-enolpyruvylshikimate phosphate synthase,
PT used to produce transgenic plants e.g. banana, wheat, maize or rice,
PT having resistance or tolerance to glyphosate herbicide.
XX
XX
PS Example 5; Page 16; 87pp; English.
XX
XX The invention relates to rice 5-enolpyruvylshikimate phosphate synthase
CC (EPSPS) genomic DNA (AAC87162). The invention also relates to an
CC expression cassette comprising, in the 5'-3' direction, one or more
CC transcriptional enhancer elements selected from AAC87190-GB7196), the
CC rice EPSPS promoter, genomic DNA encoding a rice EPSPS chloroplast
CC transit peptide, genomic DNA encoding a EPSPS protein modified such that
CC it is resistant to glyphosate (AAC87169), and a transcriptional
CC terminator. The glyphosate resistant EPSPS contains a region (AAB29793)
CC containing two amino acid substitutions relative to the corresponding
CC wild-type region (AAB29792). The invention also encompasses plant genomic
CC EPSPS sequences identified via screening with a rice EPSPS intronic
CC sequence; vectors and host plant cells comprising a nucleic acid sequence
CC of the invention; transgenic plants (and tissues and seeds thereof)
CC comprising a nucleic acid sequence of the invention, optionally further
CC transformed with a DNA encoding an insect, fungal, viral, bacterial,
CC nematode, stress or herbicide resistance protein; and methods of
CC producing the transgenic plants of the invention. The nucleic acids and
CC constructs of the invention are used to produce a wide variety of
CC morphologically normal, glyphosate resistant plants. The glyphosate
CC resistant plants produced are particularly maize, soybean, cotton,
CC sugarcane and canola, but also other field crops, fruits and vegetables,
CC turf and forage grasses and nut-producing plants. The plants are
CC optionally resistant to insects, fungi, viruses, bacteria, nematodes,
CC stresses, desiccation and/or other herbicides. They can be used in the
CC production of a herbicidal target for the high throughput in vitro
CC screening of potential herbicides. The present sequence represents a PCR
CC primer used in an exemplification of the invention

XX
SQ Sequence 48 BP; 10 A; 16 C; 11 G; 11 T; 0 U; 0 Other;
XX
Query Match 1.3%; Score 29; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 AATCGAAGATTTCTGCACCGTTTCAC 29
DB 19 AATCGAAGATTTCTGCACCGTTTCAC 47
XX
RESULT 15
ABL32090 standard; DNA; 12733 BP.
XX
AC ABL32090;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 63.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KM antileukemic; anti-HIV; anticonvulsant; ophthalmological;
KM neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KM antileukemic; antiasthmatic; antidiabetic; antipsoriatic;
KM antileukemic; cancer; eye disease; arteriosclerosis; anaemia;
KM acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KM neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KM ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
XX Claim 1; SEQ ID NO 63; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/vulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 12733 BP; 3312 A; 295 C; 3342 G; 5784 T; 0 U; 0 Other;
XX
Query Match 1.2%; Score 27; DB 6; Length 12733;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 333 AAGAGATTTTCTTTTAAAAAAA 359
DB 1915 AAGAGATTTTCTTTTAAAAAAA 1941

Search completed: April 21, 2006, 09:46:52
Job time : 1226 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2006, 09:13:40 ; Search time 8834 Seconds

(without alignments)
11625.271 Million cell updates/sec

Title: US-10-541-315-1

Perfect score: 2195
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Scoring table: 61660_NUC

Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size: 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST: *
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsa1:*
10: gb_gsa2:*
11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	465	21.2	894	10 AG832683	AG832683 Oryza sat
2	394	17.9	775	9 AQ871933	AQ871933 nbe0045B
3	291	13.3	716	1 AU075848	AU075848 AU075848
4	227	10.3	627	6 CF304397	CF304397 ABR1--04-
5	212	9.7	619	6 CF306344	CF306344 HDAL--03-
6	203	9.2	585	7 CK038003	CK038003 41717rslc
7	178	8.1	578	6 CF303311	CF303311 ABR1--01-
8	148	6.7	844	7 CR291032	CR291032 CR291032
9	147	6.7	848	10 AG871481	AG871481 Oryza sat
10	146	6.7	324	6 CF305170	CF305170 ABR1--06-
11	121	5.5	210	7 CF993308	CF993308 18211rslc
12	116	4.8	479	6 CF278393	CF278393 14ETL--04
13	100	4.6	288	6 CF304743	CF304743 ABR1--05-
14	90	4.1	295	7 CV731585	CV731585 FLO--05-K
15	83	3.8	982	5 BX929024	BX929024 BX929024
16	80	3.6	239	7 CK042297	CK042297 43579rslc
17	77	3.5	596	6 CF331107	CF331107 NACL--07-
18	75	3.4	557	6 CF340566	CF340566 RCL1--08-
19	75	3.4	560	6 CF338527	CF338527 RCL1--01-
20	75	3.4	677	6 CF339901	CF339901 RCL1--06-
21	75	3.4	680	6 CF328175	CF328175 NACL--02-
22	74	3.4	472	7 CV733575	CV733575 FLO--08-1

23	74	3.4	539	7 CV724966	CV724966 14SalT--0
24	74	3.4	550	6 CF280385	CF280385 14ETL--07
25	74	3.4	550	6 CF280540	CF280540 14ETL--07
26	74	3.4	552	6 CF319604	CF319604 HD--10-C1
27	74	3.4	559	6 CF277809	CF277809 14ETL--03
28	74	3.4	563	6 CF309066	CF309066 ABRF--03-B
29	74	3.4	564	6 CF278675	CF278675 14ETL--04
30	74	3.4	565	6 CF315243	CF315243 HD--04-B1
31	74	3.4	565	6 CF311926	CF311926 NACL--08-
32	74	3.4	566	6 CF281181	CF281181 14ETL--08
33	74	3.4	566	6 CF321214	CF321214 HD--12-G0
34	74	3.4	567	6 CF307781	CF307781 ABRF--01-F
35	74	3.4	624	6 CF319251	CF319251 HD--09-L0
36	73	3.3	491	7 CV730436	CV730436 FLO--03-P
37	73	3.3	562	6 CF332013	CF332013 NACL--08-
38	72	3.3	220	6 CF316654	CF316654 HD--06-A1
39	72	3.3	240	6 CF309951	CF309951 ABRF--04-F
40	72	3.3	374	6 CF281983	CF281983 14ETL--09
41	72	3.3	438	6 CF276542	CF276542 14ETL--01
42	72	3.3	465	6 CF278096	CF278096 14ETL--03
43	72	3.3	467	6 CF282366	CF282366 14ETL--09
44	72	3.3	468	6 CF278405	CF278405 14ETL--04
45	72	3.3	489	7 CV727881	CV727881 14SalT--0

ALIGNMENTS

RESULT 1
AG832683/c
LOCUS
DEFINITION
BAC clone:K0010A06_F, genomic survey sequence.
ACCESSION
AG832683
VERSION
AG832683.1 GI:55298918
KEYWORDS
GSS.
SOURCE
Oryza sativa (indica cultivar-group)
ORGANISM
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
Katagiri, S., Wu, J., Ito, Y., Karasawa, W., Shibata, M., Kanamori, H.,
Katayose, Y., Namiki, N., Matsumoto, T. and Sasaki, T.
TITLE
End Sequencing and Chromosomal in silico Mapping of BAC Clones
Derived from an indica Rice Cultivar, Kasalath
JOURNAL
Breeding Science 54, 273-279 (2004)
REFERENCE
AUTHORS
Sasaki, T., Matsumoto, T. and Wu, J.
TITLE
Direct Submission
JOURNAL
Submitted (29-OCT-2004) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki, 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7466)

COMMENT
The orientation of the sequence is from T7 side of the BAC clone.
FEATURES
source
1..894
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Kasalath"
/db_xref="taxon:39946"
/clone="K0010A06_F"

ORIGIN

Query Match 21.2%; Score 465; DB 10; Length 894;
Best Local Similarity 99.8%; Pred. No. 1.9e-213;
Matches 515; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1679 ATTCCCTGTTCTTCGATTTGCTTAGTCCGGAATTTTTCCTCAATATCTTAAAAA 1738
DB 630 ATTCCCTGTTCTTCGATTTGCTTAGTCCGGAATTTTTCCTCAATATCTTAAAAA 571

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Qy 1739 GTCACCTTCTGCTTCAGTTCATGAAATGATTCGTACAAATATGCTTTATAGCTTAT 1798
    |||||||
Db 570 GTCACCTTCTGCTTCAGTTCATGAAATGATTCGTACAAATATGCTTTATAGCTTAT 511
Qy 1799 CCGAGCTGATGTCAGTTATATAGTAATACCCCTATAGTTAGTCAGAGAAAGACTTAT 1858
    |||||||
Db 510 CCGAGCTGATGTCAGTTATATAGTAATACCCCTATAGTTAGTCAGAGAAAGACTTAT 451
Qy 1859 CCGATTTCTGATCTCCATTTTATATATATGAAATGAACTGATGATAGCACTATTCAT 1918
    |||||||
Db 450 CCGATTTCTGATCTCCATTTTATATATATGAAATGAACTGATGATAGCACTATTCAT 391
Qy 1919 TTGATATATATTTTATATATAGCTTACACCCCTCATTTATTCAGCTGAAAGCTGCAAT 1978
    |||||||
Db 390 TTGATATATATTTTATATATAGCTTACACCCCTCATTTATTCAGCTGAAAGCTGCAAT 331
Qy 1979 GAACGTCTCCCATTTTGTGTTTCAAATTCATCATGATATATCATGATATCCTCTGTA 2038
    |||||||
Db 330 GAACGTCTCCCATTTTGTGTTTCAAATTCATCATGATATATCATGATATCCTCTGTA 271
Qy 2039 TCTACCTGTAGAAGTTCTTTTGTGTTATCTTGAATGCTGTTGATACAGAAAGAAATTT 2098
    |||||||
Db 270 TCTACCTGTAGAAGTTCTTTTGTGTTATCTTGAATGCTGTTGATACAGAAAGAAATTT 211
Qy 2099 ATGAACTGTATATCGGAGATATATATCTGTTCTTATGATTCATTTCTTTGCGAG 2158
    |||||||
Db 210 ATGAACTGTATATCGGAGATATATATCTGTTCTTATGATTCATTTCTTTGCGAG 151
Qy 2159 TTCTTGATGATGCTGCACTTTCACACAGCAAGTT 2194
    |||||||
Db 150 TTCTTGATGATGCTGCACTTTCACACAGCAAGTT 115
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```
RESULT 2
AO871933/c 775 bp DNA linear GSS 03-NOV-1999
LOCUS nbeb0045B22r CUGI Rice BAC Library (EcoRI) Oryza sativa (japonica
DEFINITION cultivar-group) genomic clone nbeb0045B22r, genomic survey
sequence.
```

```
ACCESSION AO871933
VERSION AO871933.1 GI:6222384
KEYWORDS GSS.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 775)
AUTHORS Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1998)
COMMENT Contact: Wing RA
          Clemson University Genomics Institute
          100 Jordan Hall, Clemson, SC 29634, USA
          Tel: 864 656 7288
          Fax: 864 656 4293
          Email: rwing@clemson.edu
          Seq primer: GGAAACAGCTATGACATG
          Class: BAC ends
          High quality sequence start: 170
          High quality sequence stop: 311.
          Location/Qualifiers
            1..775
              /organism="Oryza sativa (japonica cultivar-group)"
              /mol_type="genomic DNA"
              /cultivar="japonica"
              /cultivar="Nipponbare"
              /db_xref="taxon:39947"
              /clone="nbeb0045B22r"
              /issue_type="leaf"
              /lab_host="E. coli DH10B"
              /clone_lib="CUGI Rice BAC Library (EcoRI)"
```

```
FEATURES
source
```

/note="vector: pBACindigo; Site 1: EcoRI; Site 2: EcoRI; Rice is the most important food crop in the world. Half of the world population, especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa. Nipponbare variety using EcoRI as the cloning enzyme. The library contains 55,296 clones with an average insert size of 121 Kb providing approximately 15 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Three high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening and can be requested from the Clemson University BAC/EST Resource Center (www.genome.clemson.edu)."

ORIGIN

```
Query Match 17.9%; Score 394; DB 9; Length 775;
Best Local Similarity 100.0%; Pred. No. 4.7e-179;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 69 AATGACCTTATATATAGCGCTGATTAATGATGTAAGAAAGTCAATCACC 128
    |||||||
Db 621 AATGACCTTATATATAGCGCTGATTAATGATGTAAGAAAGTCAATCACC 562
Qy 129 TACTTATGCGCAATCGGCTTAATTAATAAGAGTCGCTACACTGTTCCCTTA 188
    |||||||
Db 561 TACTTATGCGCAATCGGCTTAATTAATAAGAGTCGCTACACTGTTCCCTTA 502
Qy 189 GTAATTAAGTGGAAATGAATCATTTATGCTTGAATATPACCTCATCTGTAT 248
    |||||||
Db 501 GTAATTAAGTGGAAATGAATCATTTATGCTTGAATATPACCTCATCTGTAT 442
Qy 249 GAAGTTAAATATTCGAGGATGACCATTAATTCATCAAACTCTTGAATTAATAATC 308
    |||||||
Db 441 GAAGTTAAATATTCGAGGATGACCATTAATTCATCAAACTCTTGAATTAATAATC 382
Qy 309 TTTCTAGCTGAACCTCAATGCGGTAAGAGATATTTTTTAAATAAATAATGATGA 368
    |||||||
Db 381 TTTCTAGCTGAACCTCAATGCGGTAAGAGATATTTTTTAAATAAATAATGATGA 322
Qy 369 GATATTTGAAGCTATCGGCAAAAGTTTAAACATATATATATTTATAGTTGTG 428
    |||||||
Db 321 GATATTTGAAGCTATCGGCAAAAGTTTAAACATATATATATTTATAGTTGTG 262
Qy 429 CATTCCTATATCGCAGCTCATTTAAGACATGTC 462
    |||||||
Db 261 CATTCCTATATCGCAGCTCATTTAAGACATGTC 228
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```
RESULT 3
AU075848 716 bp mRNA linear EST 03-APR-2002
LOCUS AU075848 Rice mature leaf Oryza sativa (japonica cultivar-group)
DEFINITION cDNA clone S20385_1A, mRNA sequence.
```

```
ACCESSION AU075848
VERSION AU075848.1 GI:5455455
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 716)
AUTHORS Yamamoto, K. and Sasaki, T.
TITLE Rice cDNA from mature leaf
JOURNAL Unpublished (1999)
```


COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaka@abdr.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/
PROJECT = RGP

FEATURES
source
Location/Qualifiers
1. 716
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S20385_1A"
/cissue_type="mature leaf"
/clone_lib="Rice mature leaf"

ORIGIN

Query Match 13.3%; Score 291; DB 1; Length 716;
Best Local Similarity 99.4%; Pred. No. 3,7e-129;
Matches 511; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1216 TTGATTTTGGAAAGGGGATCTGTATCTGTGATGATTCCTGTTCTTGATTTGGATAGA 1275
|||||
DB 140 TTGATTTTGGAAAGGGGATCTGTATCTGTGATGATTCCTGTTCTTGATTTGGATAGA 199
1276 GGGGCTCTGATGTTGATGTTATCGGTTGCGTTGATTAGTAGTAGTAGTTTCAATCGT 1335
200 GGGGCTCTGATGTTGATGTTATCGGTTGCGTTGATTAGTAGTAGTAGTTTCAATCGT 259

QY 1336 CTGAGAGCTCTATGGAATGAATGTTAGGGTACGGAATCTTGCGATTTTGTAGTA 1395
|||||
DB 260 CTGAGAGCTCTATGGAATGAATGTTAGGGTACGGAATCTTGCGATTTTGTAGTA 319
1396 CCTTTTGTGAGTTAAATCAGAGCACCGGTGATTTTGTGTTGTTGTTAAAGTACAT 1455
|||||
DB 320 CCTTTTGTGAGTTAAATCAGAGCACCGGTGATTTTGTGTTGTTGTTAAAGTACAT 378
1456 TTGTTGGCTCGATTCGTGATGATGCTTCTCGATTTGACGAAGCTATCCTTGTGT 1515
|||||
DB 379 TTGTTGGCTCGATTCGTGATGATGCTTCTCGATTTGACGAAGCTATCCTTGTGT 438
1516 ATTCCCTATGGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATGATGAAG 1575
439 ATTCCCTATGGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATGATGAAG 498
1576 ATTGATTTTAAAGCTGTCGCAAAATTTCCGACGTGCTGTTGATGATGATGATGAT 1635
499 ATTGATTTTAAAGCTGTCGCAAAATTTCCGACGTGCTGTTGATGATGATGATGAT 558
1636 TCACGAAATTCATGAAGAAAGATTAATCTCGACGAACAGGGGATTCCTGTTCCCA 1695
559 TCACGAAATTCATGAAGAAAGATTAATCTCGACGAACAGGGGATTCCTGTTCCCA 618
QY 1696 TTGCTTTAGTCCCAAGATTTTTCCTCCCAATA 1729
|||||
DB 619 TTGCTTTAGTCCCAAGATTTTTCCTCCCAATA 652

RESULT 4
CF304397 627 bp mRNA 1linear EST 15-AUG-2003
LOCUS
DEFINITION ABFL--04-N21.g1 ABF3-overexpressing transgenic rice lambda phage
CDNA library (ABFL) Oryza sativa (japonica cultivar-group) cDNA
clone ABFL--04-N21, mRNA sequence.
ACCESSION
VERSION CF304397
KEYWORDS
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS 1 (bases 1 to 627)
TITLE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
JOURNAL Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1. 627
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
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/cissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABFL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match 10.3%; Score 227; DB 6; Length 627;
Best Local Similarity 99.3%; Pred. No. 3.8e-98;
Matches 447; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1216 TTGATTTTGGAAAGGGGATCTGTATCTGTGATGATTCCTGTTCTTGATTTGGATAGA 1275
179 TTGATTTTGGAAAGGGGATCTGTATCTGTGATGATTCCTGTTCTTGATTTGGATAGA 238
1276 GGGGCTCTGATGTTGATGTTATCGGTTGCGTTGATTAGTAGTAGTAGTTTCAATCGT 1335
239 GGGGCTCTGATGTTGATGTTATCGGTTGCGTTGATTAGTAGTAGTAGTTTCAATCGT 298
1336 CTGAGAGCTCTATGGAATGAATGTTAGGGTACGGAATCTTGCGATTTTGTAGTA 1395
299 CTGAGAGCTCTATGGAATGAATGTTAGGGTACGGAATCTTGCGATTTTGTAGTA 358
1396 CCTTTTGTGAGTTAAATCAGAGCACCGGTGATTTTGTGTTGTTGTTAAAGTACAT 1455
359 CCTTTTGTGAGTTAAATCAGAGCACCGGTGATTTTGTGTTGTTGTTAAAGTACAT 417
1456 TTGTTGGCTCGATTCGTGATGATGCTTCTCGATTTGACGAAGCTATCCTTGTGT 1515
418 TTGTTGGCTCGATTCGTGATGATGCTTCTCGATTTGACGAAGCTATCCTTGTGT 477
1516 ATTCCCTATGGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATGATGAAG 1575
478 ATTCCCTATGGAACAAATAATCAACTTTGAAGACGGTCCGTTGATGATGATGAAG 537
1576 ATTGATTTTAAAGCTGTCGCAAAATTTCCGACGTGCTGTTGATGATGATGATGAT 1635
538 ATTGATTTTAAAGCTGTCGCAAAATTTCCGACGTGCTGTTGATGATGATGATGAT 597
1636 TCACGAAATTCATGAAGAAAGATTAATCTCGACGAACAGGGGATTCCTGTTCCCA 1665
598 TCACGAAATTCATGAAGAAAGATTAATCTCGACGAACAGGGGATTCCTGTTCCCA 627

RESULT 5
CF306344 619 bp mRNA 1linear EST 15-AUG-2003
LOCUS

DEFINITION HDAl-03-109.g1 OshDACL1-overexpressing transgenic rice lambda phage
CDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA
clone HDAl--03-109, mRNA sequence.
ACCESSION CF306344
VERSION CF306344.1 GI:33678105
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 619)
Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.U., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE JOURNAL
AUTHORS
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
location/Qualifiers
FEATURES
source
1. 619
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39347"
/clone="HDAl-03-109"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDACL1-overexpressing transgenic rice lambda
phage CDNA library I (HDAl)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. CDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

ORIGIN
Query Match 9.7%; Score 212; DB 6; Length 619;
Best Local Similarity 99.3%; Pred. No. 7.1e-91;
Matches 432; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Oy 1216 TTGATGTAGGAAGAGGATCTGTATCTGTATGATTCCTGTCTTGGATTGGATGA 1275
Db 186 TTGATGTAGGAAGAGGATCTGTATCTGTATGATTCCTGTCTTGGATTGGATGA 245
Oy 1276 GGGGTTCTTGATGTGATGATTCGATCGGTTGATTAGTAGTAGTGTTCATCGT 1335
Db 246 GGGGTTCTTGATGTGATGATTCGATCGGTTGATTAGTAGTAGTGTTCATCGT 305
Oy 1336 CTGGAAGCTCTATGAAATGAATGTTAGGATCGGAATCTTGCGATTTTGTGAGTA 1395
Db 306 CTGGAAGCTCTATGAAATGAATGTTAGGATCGGAATCTTGCGATTTTGTGAGTA 365
Oy 1396 CCTTTGTTAGGATGAATCAAGACACCGGTGATTTGCTGGTGAATTAATAATACAT 1455
Db 366 CCTTTGTTAGGATGAATCAAGACACCGGTGATTTGCTGGTGAATTAATAATACAT 424
Oy 1456 TTGTTGGTCTCGATTCTGTAGTAGATCTTCGATTGACGAAGCTATCCTTTGTTT 1515
Db 425 TTGTTGGTCTCGATTCTGTAGTAGATCTTCGATTGACGAAGCTATCCTTTGTTT 484
Oy 1516 ATTCCCTATGAAACAAATAATCAACTTTGAAGACGGTCCGTTGATGAGATTGAATG 1575
Db 485 ATTCCCTATGAAACAAATAATCAACTTTGAAGACGGTCCGTTGATGAGATTGAATG 544
Oy 1576 ATTGATTTCTTAAGCTCTGCCAAATTTGCGACACTGGCTTTTAATACAGTAGCCCCA 1635
Db 545 ATTGATTTCTTAAGCTCTGCCAAATTTGCGACACTGGCTTTTAATACAGTAGCCCCA 604

Oy 1636 TCACGAATTCATGA 1650
Db 605 TCACGAATTCATGA 619

RESULT 6
CK038003
LOCUS
DEFINITION 41717rcicg 14440.Y1 Oryza sativa cv. 93-11 tillering whole plant
CDNA library Oryza sativa cDNA 5', mRNA sequence.
ACCESSION CK038003
VERSION CK038003.1 GI:58609970
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 585)
Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Lin,L., Yin,J., Geng,J., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Zhang,J., Zhang,Y., Li,G., Shi,J., Liu,J.,
Ly,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
The Genomes of Oryza sativa: A History of Duplications
PLoS Biol. 3 (2), e38 (2005)
15685292
TITLE JOURNAL
AUTHORS
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 585
POLYA=No.
location/Qualifiers
FEATURES
source
1. 585
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="93-11"
/db_xref="taxon:4530"
/tissue_type="whole plant"
/dev_stage="tillering"
/clone_lib="Oryza sativa cv. 93-11 tillering whole plant
CDNA library"

ORIGIN
Query Match 9.2%; Score 203; DB 7; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1167 CCTTCGGTGTCTTGATTTATGTTCTAGTGTGTAGTACGGGGTGTAGTGA 1226
Db 143 CCTTCGGTGTCTTGATTTATGTTCTAGTGTGTAGTACGGGGTGTAGTGA 202
Oy 1227 AAAGGGATCTGATCTGTATGATTCCTGTTCTTGATTTGGATAGAGGGTCTTGA 1286
Db 203 AAAGGGATCTGATCTGTATGATTCCTGTTCTTGATTTGGATAGAGGGTCTTGA 262
Oy 1287 TGTTCATGTATGAGTTCGATTTGATTAGTAGTAGTGTTCATGTCGTGAGAGCTC 1346
Db 263 TGTTCATGTATGAGTTCGATTTGATTAGTAGTAGTGTTCATGTCGTGAGAGCTC 322
Oy 1347 TATGAAATGAATGTTTGAAGG 1369
Db 323 TATGAAATGAATGTTTGAAGG 345

RESULT 7
CF303311 578 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
ABF1--01-016-g1 ABF3-overexpressing transgenic rice lambda phage
CDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--01-016, mRNA sequence.
ACCESSION
CF303311 GI:33675072
VERSION
CF303311.1
KEYWORDS
Oryza sativa (japonica cultivar-group)
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 578)
REFERENCE
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.T., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
TITLE
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomic and Genetic Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..578
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--01-016"
/rissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage CDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match 8.1%; Score 178; DB 6; Length 578;
Best Local Similarity 99.3%; Pred. No. 2.1e-74;
Matches 398; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1216 TTGATCTTGAAGAGGAGTCTGATCTGATGATTTCCGTTCTTGATTTGGGATGAG 1275
|||||
DB 179 TTGATCTTGAAGAGGAGTCTGATCTGATGATTTCCGTTCTTGATTTGGGATGAG 238
|||||
QY 1276 GGGGTTCTGATGTTGATGATTCGTTCCGTTGATTTAGTAGTAGTTTCAATCGT 1335
|||||
DB 239 GGGGTTCTGATGTTGATGATTCGTTCCGTTGATTTAGTAGTAGTTTCAATCGT 298
|||||
QY 1336 CTGAGAGCTTATGGAATGAATGTTAGGGTACGGAATCTTCCGATTTTGTAGTA 1395
299 CTGAGAGCTTATGGAATGAATGTTAGGGTACGGAATCTTCCGATTTTGTAGTA 358
|||||
QY 1396 CCTTTTGTGAGTGAATCGAGACCGGTGATTTTGGTGTGATTTTAAAGTACAT 1455
|||||
DB 359 CCTTTTGTGAGTGAATCGAGACCGGTGATTTTGGTGTGATTTTAAAGTACAT 417
|||||
QY 1456 TTGTTGCTCTGATTTCTGATGATGCTTCTCGATTTGACGAAGCTATCCTTTGTT 1515
418 TTGTTGCTCTGATTTCTGATGATGCTTCTCGATTTGACGAAGCTATCCTTTGTT 477
|||||
QY 1516 ATTCCTTATGAAACAAATATCAACTTTGAAAGCGGTCCGTTGATGATTAAGT 1575
478 ATTCCTTATGAAACAAATATCAACTTTGAAAGCGGTCCGTTGATGATTAAGT 537
|||||

QY 1576 ATTGATTTCTTAAGCCTGTCCAAAATTTCCGACCTGGCTTGT 1616
|||||
DB 538 ATTGATTTCTTAAGCCTGTCCAAAATTTCCGACCTGGCTTGT 578
|||||

RESULT 8
CR291032 844 bp mRNA linear EST 27-FEB-2004
LOCUS
DEFINITION
CR291032 Oryza sativa library (Han B) Oryza sativa cDNA clone
Y604h07p5, mRNA sequence.
ACCESSION
CR291032 GI:44677598
VERSION
CR291032.1
KEYWORDS
EST.
SOURCE
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 844)
REFERENCE
Han,B., Feng,Q., Huang,Y.C., Yang,K., Li,Y., Guan,J.P., Zhu,J.J.,
Zhao,Q., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L.,
Weng,Q.J., Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T.,
Zhang,Y.J., Lu,Y., Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X.,
Zhang,L., Lan,L.F., Chen,W., Wu,S.A. and Xue,Y.B.
Rice cDNA EST clone
Unpublished (2003)
TITLE
JOURNAL
COMMENT
Contact: Han Bin
National Center for Gene Research
Chinese Academy of Sciences
500# Cao Bao Road, Shanghai 200233, China
Email: bhan@ncgr.ac.cn
Clone requests: bhan@ncgr.ac.cn
This is rice cDNA est clone
Web site: http://www.ncgr.ac.cn.
Location/Qualifiers
1..844
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="Y604h07p5"
/clone_lib="Oryza sativa library (Han B)"

ORIGIN
Query Match 6.7%; Score 148; DB 7; Length 844;
Best Local Similarity 100.0%; Pred. No. 7e-60;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 947 GAGGAGAGCAAGAAACCAAGATCTCTCTCCATCTATAATTCCTCCCTT 1006
24 GAGGAGAGCAAGAAACCAAGATCTCTCTCCATCTATAATTCCTCCCTT 83
|||||
QY 1007 TTCCCTCTCTATATGAGGATCCAGCCCAAGAGGAGAGCACCAGACACGCG 1066
|||||
DB 84 TTCCCTCTCTATATGAGGATCCAGCCCAAGAGGAGAGCACCAGACACGCG 143
|||||
QY 1067 ACTAGCAGAGCGGAGCGGCGGCTTCT 1094
144 ACTAGCAGAGCGGAGCGGCGGCTTCT 171
|||||

RESULT 9
AG871481 848 bp DNA linear GSS 03-NOV-2004
LOCUS
DEFINITION
AG871481 Oryza sativa (indica cultivar-group) genomic DNA, BAC end sequence,
BAC clone:K0245F03_R, genomic survey sequence.
ACCESSION
AG871481 GI:55337716
VERSION
AG871481.1
KEYWORDS
GSS.
SOURCE
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE	1	Khuramzadeh, Oryzae; Oryza.
AUTHORS	Katagiri, S., Wu, J., Ito, Y., Kanaoka, M., Shibata, M., Kanamori, H., Katsuge, Y., Namiki, N., Matsumoto, T. and Sasaki, T.	
TITLE	End Sequencing and Chromosomal in silico Mapping of BAC Clones Derived from an indica Rice Cultivar, Kasalath	
JOURNAL	Breeding Science 54, 273-279 (2004)	
REFERENCE	2 (bases 1 to 848)	
AUTHORS	Sasaki, T., Matsumoto, T. and Wu, J.	
TITLE	Direct Submission	
JOURNAL	Submitted (29-Oct-2004) Takuji Sasaki, National Institute of Agricultural Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki, 305-8602, Japan	
COMMENT	(E-mail: tsasaki@ias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)	
FEATURES	The orientation of the sequence is from SP6 side of the BAC clone.	
SOURCE	Location/Qualifiers	
ORIGIN	1..848	
Query Match	6.7%; Score 147; DB 10; Length 848;	
Best Local Similarity	100.0%; Pred. No. 2.1e-59; Mismatches 0; Indels 0; Gaps 0;	
Matches 147; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1216 TTGATGTTAGGAAAGGGGATCTGTATCTGTGATGATTCCTGTTCTGGATTGGGATGA 1275	
DB	107 TTGATGTTAGGAAAGGGGATCTGTATCTGTGATGATTCCTGTTCTGGATTGGGATGA 166	
OY	1276 GGGGTTCTTGATGTCATGTTATTCGGTTCCGTTGGATTAGTAGTTCGTTTCATTCGT 1335	
DB	167 GGGGTTCTTGATGTCATGTTATTCGGTTCCGTTGGATTAGTAGTTCGTTTCATTCGT 226	
OY	1336 CTGGAGACTCTAGGAATGAATG 1362	
DB	227 CTGGAGACTCTAGGAATGAATG 253	
RESULT 10		
CP305170		
LOCUS	CP305170 324 bp mRNA EST 15-AUG-2003	
DEFINITION	ABR1--06-P15.g1 ABR1-overexpressing transgenic rice lambda phase cDNA library (ABR1) Oryza sativa (japonica cultivar-group) cDNA	
ACCESSION	CP305170	
VERSION	CP305170.1 GI:33676931	
KEYWORDS	EST.	
SOURCE	Oryza sativa (japonica cultivar-group)	
ORGANISM	Oryza sativa (japonica cultivar-group)	
REFERENCE	1 (bases 1 to 324)	
AUTHORS	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.	
TITLE	Large-scale Sequencing Analysis of Rice ESTs	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Nahm B. H. Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University, Yongin, Kyonggi, Korea	
FEATURES	Tel: 82 31 330 6193	
SOURCE	Fax: 82 31 321 6355	
ORIGIN	Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.	
ORIGIN	Location/Qualifiers	
1..324		
/organism="Oryza sativa (japonica cultivar-group)"		
/mol_type="mRNA"		
/db_xref="taxon:39946"		
/clone="K0245F03_R"		

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/db_xref="taxon:39947"
/clone="ABR1--06-P15"
/tissue_type="leaf"
/issue="14 days after germination"
/lab_host="E.coli SOLR"
/clone_id="ABR3-overexpressing transgenic rice lambda
phage cDNA library (ABR1)"
/node="vector: pluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match      6.7%; Score 146; DB 6; Length 324;
Best Local Similarity 100.0%; Pred. No. 7e-59;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1216  TTGATGTTAGAAAGGGGATCTGATCTGATGATGATTCCTGTTCTTGATTTGGATATGA 1275
DDB      179  TTGATGTTAGAAAGGGGATCTGATCTGATGATGATTCCTGTTCTTGATTTGGATATGA 238
OY      1276  GGGGTTCTTGATGTTGATGTTATCGGTTGATTTAGTAGATGATGTTTCAATCGT 1335
DDB      239  GGGGTTCTTGATGTTGATGTTATCGGTTGATTTAGTAGATGATGTTTCAATCGT 298
OY      1336  CTGAGAGCCTCTATGAAATGAATG 1361
DDB      299  CTGAGAGCCTCTATGAAATGAATG 324

RESULT 11
LOCUS   CF993308
DEFINITION 18211rsicee.g317.y1 Oryza sativa cv. LYP9 cilleering whole plant
cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA
sequence.
ACCESSION CF993308
VERSION   CF993308.1 GI:58595000
KEYWORDS  EST.
SOURCE    Oryza sativa (indica cultivar-group)
ORGANISM  Oryza sativa (indica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharctoidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 210)
AUTHORS   Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,X., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ran,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
TITLE     The Genomes of Oryza sativa: A History of Duplications
JOURNAL   PLOS Biol. 3 (2), e38 (2005)
COMMENT   PUBMED
15685292
Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 210
POLY(A=No.

FEATURES
Source
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/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="LYP9"
/db_xref="taxon:39946"

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ORIGIN

/issue_type="whole plant"
/dev_stage="tillering"
/clone_1ib="Oryza sativa cv. Lyp9 tillering whole plant
cDNA library"

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Best Local Similarity 100.0%; Pred. No. 9.3e-47;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 974 CTCCTCTCCCACTATAATTCCTCCCTTTCCCTCTCTATATAGAGGCAATCA 1033

DB 9 CTCCTCTCCCACTATAATTCCTCCCTTTCCCTCTCTATATAGAGGCAATCA 68

QY 1034 ACCCAAGAGAGGAGAGACCAAGACGACGACTAGAGAAAGCCGAGCGGCTTC 1093

DB 69 ACCCAAGAGAGGAGAGACCAAGACGACGACTAGAGAAAGCCGAGCGGCTTC 128

QY 1094 T 1094

DB 129 T 129

RESULT 12 479 bp mRNA linear EST 14-AUG-2003
CF278393
LOCUS 14ETL--04-R15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-R15,
mRNA sequence.

ACCESSION CF278393.1 GI:33655779

VERSION CF278393

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source 1.479
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="14ETL--04-R15"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_1ib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Query Match 4.8%; Score 106; DB 6; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 986 TCTATAAATTCCTCCCTTTTCCCTCTCTATATAGAGGACATCAAGCAAGAG 1045

DB 83 TCTATAAATTCCTCCCTTTTCCCTCTCTATATAGAGGACATCAAGCAAGAG 142

QY 1046 GGAGAGCACCAAGACACGCGACTAGACAGACCCGACCGCCT 1091

DB 143 GGAGAGCACCAAGACACGCGACTAGACAGACCCGACCGCCT 188

RESULT 13 288 bp mRNA linear EST 15-AUG-2003
CF304743
LOCUS ABF1--05-N05.g1 ABF3-overexpressing transgenic rice lambda phage
DEFINITION cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--05-N05, mRNA sequence.

ACCESSION CF304743

VERSION CF304743.1 GI:33676504

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source 1.288
Location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--05-N05"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_1ib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN

Query Match 4.6%; Score 100; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.4e-36;
Matches 100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1216 TTGATGTAGAGAAAGGATCGTATCTGTATGATGATTCCTGTTGGATTGGATAGA 1275

DB 179 TTGATGTAGAGAAAGGATCGTATCTGTATGATGATTCCTGTTGGATTGGATAGA 238

QY 1276 GGGGTTCTTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1315

DB 239 GGGGTTCTTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 278

RESULT 14

CV731585 295 bp mRNA linear EST 05-NOV-2004

LOCUS FLO--05-K23.b1 Rice flower lambda phage cDNA library (FLO) Oryza

DEFINITION sativa (japonica cultivar-group) cDNA clone FLO--05-K23, mRNA

ACCESSION CV731585

VERSION CV731585.1 GI:55436839

Oy	333	AGAGAGATTTTTTTTTTAAAAAAAATGAATGAAGAATTTCTGAACGATCGGCAAG	3922
Dd	334	AGAGAGATTTTTTTTTT---AAAAAATGAAATGAAGATTTCTGAACGATCGGCAAG	390
Oy	393	ATTAAACATATATATATATATATTTATATAGTTGTGCATTGCTATATCGCACGTCTTA	4522
Dd	391	ATTAAACATATATATATATATATTTATATAGTTGTGCATTGCTATATCGCACGTCTTA	450
Oy	433	AGGACATGCTTACTCTCATCTCAATTTTTTATTAGTATATTAAGACAACTTGACTTATTTT	5121
Dd	451	AGGACATGCTTACTCTCATCTCAATTTTTTATTAGTATATTAAGACAACTTGACTTATTTT	510
Oy	513	TATTTATTTATCTTTTTTGATTTAGATGCAAGGTACTTAAGCACAACTTTGTGCTATGT	5722
Dd	511	TATTTATTTATCTTTTTTGATTTAGATGCAAGGTACTTAAGCACAACTTTGTGCTATGT	570
Oy	573	GCATGTGTGAGTGACACTCTCTC-ATACAGTTTCMACTAGGACACATCTTCCATATCACT	6311
Dd	571	GCATGTGTGAGTGACACTCTCTCAATACAGTTTCMACTAGGACACATCTTATATCACT	630
Oy	632	CGCCTATTTAATACATTTNAGTNGACAAATCTGAATTCAGACCTTCACATCACAGAC	691
Dd	631	CGCCTATTTAATACATTTNAGTNGACAAATCTGAATTCAGACCTTCACATCACAGAC	690
Oy	692	CACCTTTAATATATCTAATAAATACAAAATAATTTTACAGATATAGATGAANAAGTATGA	751
Dd	691	CACCTTTAATATATCTAATAAATACAAAATAATTTTACAGATATAGATGAANAAGTATGA	750
Oy	752	AACGAACCTAATNAGTTTTTTCACATACAAAAAAAAGATTTTGTCTGTGCGGAGCG	8111
Dd	751	AACGAACCTAATNAGTTTTTTCACATACAAAAAAAAGATTTTGTCTGTGCGGAGCG	810
Oy	812	CCAATCTCCCATATTTGGGACACAGGCAACACAGAGTGGCTGCCACAGAACATCCAC	8711
Dd	811	CCAATCTCCCATATTTGGGACACAGGCAACACAGAGTGGCTGCCACAGAACATCCAC	870
Oy	872	AAAAAACGATGATCTTAACGAGAGACAGC	899
Dd	871	AAAAAACGATGATCTTAACGAGAGACAGC	898

```

RESULT 2
US-10-012-070A-17
Sequence 17, Application US/10012070A
Patent No. 6867293
GENERAL INFORMATION:
APPLICANT: Hawkes, Timothy
APPLICANT: Warner, Simon
APPLICANT: Andrews, Christopher
APPLICANT: Bachoo, Satvinder
APPLICANT: Pickrell, Andrew
TITLE OF INVENTION: Herbicide Resistant Plants
FILE REFERENCE: 50490/UST
CURRENT APPLICATION NUMBER: US/10/012,070A
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/GB00/01573
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-17

```

Query Match	1.3%	Score 29	DB 3	Length 48
Best Local Similarity	100.0%	Pred. No. 0.0063		
Matches 29	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 AATCGAAAAGTTTCTGCACCGTTTCAC	29		

[illegible]

```

RESULT 4
US-10-349-782-6/c
: Sequence 6, Application US/10349782
: Patent No. 6955882
: GENERAL INFORMATION:
: APPLICANT: Yves Hatzfeld
: APPLICANT: Valerie Marie-No. 695588211e Frankard
: APPLICANT: Anne-Marie Droual
: TITLE OF INVENTION: Method for easy cloning and selection of chimeric DNA molecules
: FILE REFERENCE: 1187-15
: CURRENT APPLICATION NUMBER: US/10/349,782
: CURRENT FILING DATE: 2003-01-23
: PRIOR APPLICATION NUMBER: EP 02075373.7
: PRIOR FILING DATE: 2002-01-23
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 6
: LENGTH: 22
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Primer 2432 (N1)
US-10-349-782-6

```

	Query	Match	Similarity	Score	DB	Length	Mismatches	Indels	Gaps
	Best Local	22	100.0%	100.0%	3	22	0	0	0
	Conervative	22	0	0	3	22	0	0	0
Qy	2174 GCCACTTTCCACGCAAGTTC	2195							
Db	22 GCCACTTTCCACGCAAGTTC	1							

RESULT 5
US-10-012-070A-18/c
; Sequence 18, Application US/10012070A


```
; Patent No. 6867293
; GENERAL INFORMATION:
; APPLICANT: Hawkes, Timothy
; APPLICANT: Warner, Simon
; APPLICANT: Andrews, Christopher
; APPLICANT: Bachoo, Savinder
; APPLICANT: Pickrell, Andrew
; TITLE OF INVENTION: Herbicide Resistant Plants
; FILE REFERENCE: 50490/UST
; CURRENT APPLICATION NUMBER: US/10/012,070A
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: PCT/GB00/01573
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 18
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-18

Query Match          1.0%; Score 22; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      878 CGATGATCTAACGAGAGACG 899
DB      36 CGATGATCTAACGAGAGACG 15

RESULT 6
US-09-949-016-13185/C
; Sequence 13185, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13185
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13185

Query Match          1.0%; Score 22; DB 3; Length 251769;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 AAAATACAAAAAATATTAC 730
DB      119547 AAAATACAAAAAATATTAC 119526

RESULT 7
US-09-949-016-13186/C
; Sequence 13186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
```

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13186
; LENGTH: 251769
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13186

Query Match          1.0%; Score 22; DB 3; Length 251769;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 AAAATACAAAAAATATTAC 730
DB      119547 AAAATACAAAAAATATTAC 119526

RESULT 8
US-09-949-016-13187/C
; Sequence 13187, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13187
; LENGTH: 266748
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13187

Query Match          1.0%; Score 22; DB 3; Length 266748;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      709 AAAATACAAAAAATATTAC 730
DB      119512 AAAATACAAAAAATATTAC 119491

RESULT 9
US-09-949-016-13188/C
; Sequence 13188, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```

;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13188
;; LENGTH: 266748
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13188

Query Match 1.0%; Score 22; DB 3; Length 266748;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 AAAATTCAGAAAATTAATTTTAC 730
DB 119512 AAAATTCAGAAAATTAATTTTAC 119491

RESULT 10
US-09-423-233-18
; Sequence 18, Application US/09423233
; Patent No. 6372430
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Nucleic Acids for Detecting Aspergillus Species and
; FILE REFERENCE: 03063-0341MP
; CURRENT APPLICATION NUMBER: US/09/423,233
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 360
; TYPE: DNA
; ORGANISM: Rhizopus circinans
US-09-423-233-18

Query Match 1.0%; Score 21; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 ATATTTTAAAAA 359
DB 125 ATATTTTAAAAA 145

RESULT 11
US-09-533-559-1048
; Sequence 1048, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849-200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1048
; LENGTH: 487
; TYPE: DNA

;; ORGANISM: Fusarium venenatum
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (1)...(487)
;; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1048

Query Match 1.0%; Score 21; DB 3; Length 487;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 342 TTTTAAAAAATAG 362
DB 31 TTTTAAAAAATAG 51

RESULT 12
US-09-949-016-187814/C
; Sequence 187814, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187814
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187814

Query Match 1.0%; Score 21; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TTTTAAAAAATAGA 363
DB 328 TTTTAAAAAATAGA 308

RESULT 13
US-09-016-434-1156
; Sequence 1156, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Selhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1156:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1531982
US-09-016-434-1156

```

```

Query Match      1.0%; Score 21; DB 3; Length 813;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      339 ATATTTTTTTTTTAAAAAAA 359
Db      479 ATATTTTTTTTTTAAAAAAA 499

```

```

RESULT 14
US-09-843-472-2
Sequence 2, Application US/09843472
Patent No. 6544783
GENERAL INFORMATION:
APPLICANT: Pereira, J. Ranjan
APPLICANT: Lu, Min
TITLE OF INVENTION: Polynucleotide Sequences from Rice
FILE REFERENCE: AKK-103C5XC1
CURRENT APPLICATION NUMBER: US/09/843,472
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,870
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/217,891
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/218,366
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/227,231
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/237,736
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/253,925
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 938
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(938)
OTHER INFORMATION: n = a, c, g, or t.
US-09-843-472-2

```

```

Query Match      1.0%; Score 21; DB 3; Length 938;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      341 ATTTTTTTTTTAAAAAATA 361
Db      185 ATTTTTTTTTTAAAAAATA 205

```

```

RESULT 15
US-09-843-472-2/c
Sequence 2, Application US/09843472
Patent No. 6544783
GENERAL INFORMATION:
APPLICANT: Pereira, J. Ranjan
APPLICANT: Lu, Min
TITLE OF INVENTION: Polynucleotide Sequences from Rice
FILE REFERENCE: AKK-103C5XC1
CURRENT APPLICATION NUMBER: US/09/843,472
PRIOR FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: 60/199,870
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/217,891
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/218,366
PRIOR FILING DATE: 2000-07-13
PRIOR APPLICATION NUMBER: 60/227,231
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/237,736
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/253,925
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 938
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(938)
OTHER INFORMATION: n = a, c, g, or t.
US-09-843-472-2

```

```

Query Match      1.0%; Score 21; DB 3; Length 938;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      340 TATTTTTTTTTTAAAAAAT 360
Db      205 TATTTTTTTTTTAAAAAAT 185

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Search completed: April 21, 2006, 09:21:42
Job time : 403 secs

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QY	DB	Sequence	Score	DB	Length	Matches	Conservative	Indels	Gaps
QY	DB	274 ATAAATTCGATCGAAACCTCTCTGTAATAAATAAAATCTTCTAGCTGAAGCTCAATGGGTAA	18.3%	33	92	862	0	2	2
QY	DB	333 AGAGAGATATTTTTTTTTTTTAAAAAAATATGAAATGAAAGATATTTCTGAACGTATCGCAAA	18.3%	33	92	862	0	2	2
QY	DB	334 AGAGAGATATTTTTTTTTT--AAAAAAATGAAATGAAATATTTCTGAACGTATCGCAAA	18.3%	33	92	862	0	2	2
QY	DB	393 ATTTAAACATATTAATTAATTAATTTATATGTTTGAAGTTCGTTATATGCAAGCTATTA	18.3%	33	92	862	0	2	2
QY	DB	391 ATTTAAACATATTAATTAATTAATTTATATGTTTGAAGTTCGTTATATGCAAGCTATTA	18.3%	33	92	862	0	2	2
QY	DB	453 AGGACATGCTTACTCTCCATCTCCAAATTTTATTTAGTAAATTAAGCAATTTGACTTATTTT	18.3%	33	92	862	0	2	2
QY	DB	451 AGGACATGCTTACTCTCCATCTCCAAATTTTATTTAGTAAATTAAGCAATTTGACTTATTTT	18.3%	33	92	862	0	2	2
QY	DB	513 TATTATTTATCTTTTTTGGATTAGATGCAAGTACTTACGACACACTTTGTCTCATGT	18.3%	33	92	862	0	2	2
QY	DB	511 TATTATTTATCTTTTTTGGATTAGATGCAAGTACTTACGACACACTTTGTGTCTCATGT	18.3%	33	92	862	0	2	2
QY	DB	573 GCATGTGTGAGCGACCTCTTC--ATACAGCTTCACTGACGACACATCTCCAAATTTGACT	18.3%	33	92	862	0	2	2
QY	DB	571 GCATGTGTGAGCGACCTCTTC--ATACAGCTTCACTGACGACACATCTCCAAATTTGACT	18.3%	33	92	862	0	2	2
QY	DB	632 CGCCATTTTAAATACATTTAGTAGGCAATATCTGAATTCGAAGCACTTCCATCACCAGAC	18.3%	33	92	862	0	2	2
QY	DB	631 CGCCATTTTAAATACATTTAGTAGGCAATATCTGAATTCGAAGCACTTCCATCACCAGAC	18.3%	33	92	862	0	2	2
QY	DB	692 CACTTTTAAATATATCTTAAATATACAAAAATATTTTACAGATATGATGAAATAGATGA	18.3%	33	92	862	0	2	2
QY	DB	691 CACTTTTAAATATATCTTAAATATACAAAAATATTTTACAGATATGATGAAATAGATGA	18.3%	33	92	862	0	2	2
QY	DB	752 AACGAACATTTTAGTTTTTTCATATACAAAAAAATTTTGTCTGTGCGGAGACG	18.3%	33	92	862	0	2	2
QY	DB	751 AACGAACATTTTAGTTTTTTCATATACAAAAAAATTTTGTCTGTGCGGAGACG	18.3%	33	92	862	0	2	2
QY	DB	812 CCAATCTCCCATATTTGGGACACAGAGCAACAGAGTGGCTGCCACAGAAACAACCCAG	18.3%	33	92	862	0	2	2
QY	DB	811 CCAATCTCCCATATTTGGGACACAGAGCAACAGAGTGGCTGCCACAGAAACAACCCAG	18.3%	33	92	862	0	2	2
QY	DB	872 AAAAAACGATGATCTTACGAGAGCAGC	18.3%	33	92	862	0	2	2
QY	DB	871 AAAAAACGATGATCTTACGAGAGCAGC	18.3%	33	92	862	0	2	2
QY	DB	871 AAAAAACGATGATCTTACGAGAGCAGC	18.3%	33	92	862	0	2	2

Db 34 TTAACCTAACCAATATATGAGGAACGATGCTGAATATATTAATGAGACCTTATATATGACGC 93

Qy 93 TGATTAACCTAGAACTATATGTAAGAAAACTATCATCACTTATGTCGCAATCGGGCTTAA 152

Db 94 TGATTAACCTAGAACTATATGTAAGAAAACTATCATCACTTATGTCGCAATCGGGCTTAA 153

Qy 153 TAAAAAAGAGTGCCTACACTAGTGTGTTGCTTCTTGTATTAATGAGGAAAAATGAATC 212

Db 154 TAAAAAAGAGTGCCTACACTAGTGTGTTGCTTCTTGTATTAATGAGGAAAAATGAATC 213

Qy 213 ATTATGCTTGAATAATATACGTTCAACATCTCTGTCATGAAGTTAAATTTGAGGTAGCC 272

Db 214 ATTATGCTTGAATAATATACGTTCAACATCTCTGTCATGAAGTTAAATTTGAGGTAGCC 273

Qy 273 ATAAATGTCATCAAACTCTTCTTGGAATTAATAAATCTTTCTAGCTCAACTCAATGGGTAA 333

Db 274 ATAAATGTCATCAAACTCTTCTTGGAATTAATAAATCTTTCTAGCTCAACTCAATGGGTAA 333

Qy 333 AGAGGATATATTTTAAAAAATGAAATGAAATATTCGTGAACGATCGGCAAG 392

Db 334 AGAGGATATATTTTAAAAAATGAAATGAAATATTCGTGAACGATCGGCAAG 390

Qy 393 ATTTAAACATATTAATTAATTAATTTTATGTTTGATTTGCTTATATGCAAGTCAATTA 452

Db 391 ATTTAAACATATTAATTAATTAATTTTATGTTTGATTTGCTTATATGCAAGTCAATTA 450

Qy 453 AGGACATGCTTATCTCCATCTCAATTTTATTTAGTAATTAAGAACAATTGACTATTTT 512

Db 451 AGGACATGCTTATCTCCATCTCAATTTTATTTAGTAATTAAGAACAATTGACTATTTT 510

Qy 513 TATTAATTAATCTTTTGGATAGATGCAAGGACTTAGGACACACTTGTGCTCATGT 572

Db 511 TATTAATTAATCTTTTGGATAGATGCAAGGACTTAGGACACACTTGTGCTCATGT 570

Qy 573 GCATGTGAGTGCACCTCTCTC-ATACAGCTTCAACTAGCGACACATCTTCCAATATCACT 631

Db 571 GCATGTGAGTGCACCTCTCTC-ATACAGCTTCAACTAGCGACACATCTTCCAATATCACT 630

Qy 632 CGCCTATTTAATACATTTAGTAGGCAATATCTGAATTCAAGCACTCACCATCAACCGAC 691

Db 631 CGCCTATTTAATACATTTAGTAGGCAATATCTGAATTCAAGCACTCACCATCAACCGAC 690

Qy 692 CACTTTTAATTAATCTAATAATACAAAAATTAATTTTACAGAAATAGCAATGAAGTGA 751

Db 691 CACTTTTAATTAATCTAATAATACAAAAATTAATTTTACAGAAATAGCAATGAAGTGA 750

Qy 752 AACGAACTATTTAGGTTTTCACATACAAAAAAGATTTTCTCGTCGCGGACG 811

Db 751 AACGAACTATTTAGGTTTTCACATACAAAAAAGATTTTCTCGTCGCGGACG 810

Qy 812 CCAATCTCTCCATATTTGGGACACAGGCAACAACAAGTGGCTGCGCAACAACCCAC 871

Db 811 CCAATCTCTCCATATTTGGGACACACAGGCAACAACAAGTGGCTGCGCAACAACCCAC 870

Qy 872 AAAAAACGATGATCTTAACGAGGACAGC 899

Db 871 AAAAAACGATGATCTTAACGAGGACAGC 898

RESULT 3

US-10-437-963-33718

Sequence 33718, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;
; FILE REFERENCE: 38-21(53221) B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
;
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33718
;
; LENGTH: 762
;
; TYPE: DNA
;
; ORGANISM: Oryza sativa
;
; FEATURE:
;
; NAME/KEY: unsure
; LOCATION: (1)..(762)
; OTHER INFORMATION: unsure at all n locations
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: PAT_MHT4530_37802C.1
;
US-10-437-963-33718

```

Query Match	13.3%	Score 291	DB 7	Length 762
Best Local Similarity	99.4%	Pred. No.	1.7e-130	
Matches 511; Conservative	0	Mismatches	2	Indels 1; Gaps 1

Qy	1216	TTGATGCTTAGGAAGAGGAGCTGTAATCTGTGATGATGATCTGTTCTTGGATTTGGATAGA	1275
Db	186	TTGATGCTTAGGAAGAGGAGCTGTAATCTGTGATGATGATCTGTTCTTGGATTTGGATAGA	245
Qy	1276	GGGGTCTTGATGTCAGATGTAATCGTTCGGTTGATTTAGTAGATGTTTCAATCGT	1339
Db	246	GGGGTCTTGATGTCAGATGTAATCGTTCGGTTGATTTAGTAGATGTTTCAATCGT	305
Qy	1336	CTGAGAGCTCTATGGAATGAATGTTTAGGCTAGCGAATCTTGCATTTTGTAGTA	1399
Db	306	CTGAGAGAGCTCTATGGAATGAATGTTTAGGAGATCGGAATCTTGCATTTTGTAGTA	365
Qy	1396	CCTTTTGTTTAGAGTAATAACAGACACCGGTGATTTTGCTGGTGTAATAAAGTAAT	1455
Db	366	CCTTTGTGTTTAGAGTAATAACAGACACCGGTGATTTTGCTGGTGTAAT-AAAGTAAT	424
Qy	1456	TTGTTGGTCCCGATCTCGTAGTAGATGATCTTCGATTTGACGAGCATCCTTGGTT	1515
Db	425	TTGTTGGTCCCGATCTCGTAGTAGATGATCTTCGATTTGACGAGCATCCTTGGTT	484
Qy	1516	ATTCCCTATTGAACAAAATAATATCAACTTTGAGAAGCGGTCCCGTTGATGATTTGAATG	1575
Db	485	ATTCCCTATTGAACAAAATAATATCAACTTTGAGAAGCGGTCCCGTTGATGATTTGAATG	544
Qy	1576	ATTGATTCCTTAGACCTGTCCAAAATTTGCGAGCTGGCTTGTTAGATACAGTAGTCCCCA	1635
Db	545	ATTGATTCCTTAGACCTGTCCAAAATTTGCGAGCTGGCTTGTTAGATACAGTAGTCCCCA	604
Qy	1636	TCAGGAATTCATGAAAAAGATTATATCTTCAGGAACAAGGGGATTCCTGTGTTCCGA	1695
Db	605	TCAGGAATTCATGAAAAAGATTATATCTTCAGGAACAAGGGGATTCCTGTGTTCCGA	664
Qy	1696	TTTGCTTTAGTCCCGAATTTTTTTTCCCAATA	1729
Db	665	TTTGCTTTAGTCCCGAATTTTTTTTCCCAATA	698

RESULT 4
 US-10-437-963-7912
 ; Sequence 7912, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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; FILE REFERENCE: 38-21(53321)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 7912
; LENGTH: 3221
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14463C.1
US-10-437-963-7912

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Query Match	3.4%	Score 74;	DB 7;	Length 3221;
Best Local Similarity	100.0%	Pred. No. 8, 1e-25;		
Matches 74;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1018	ATTATGAGGCGCATCCAGGCCAAGAAGGGAGAGACCAAGGACACCGCATATGACAGAG	1077
Db	251	ATTATGAGGCGCATCCAGGCCAAGAAGGGAGAGACCAAGGACACCGCATGACAGAG	310
Oy	1078	CCGAGCGGACCGGCTT	1091
Db	311	CCGAGCGGACCGGCTT	324

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RESULT 5
US-10-487-901-2760
; Sequence 2760, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:
; APPLICANT: Oreido, Jeremiah Vincent
; APPLICANT: McCreery, David
; APPLICANT: Pell, Randy
; APPLICANT: Miller, Barbara
; APPLICANT: Weglarz, Thaddaeus
; APPLICANT: Gachotte, Daniel
; APPLICANT: Blakeslee, Beth
; APPLICANT: Larrinna, Ignacio
; APPLICANT: Reddy, Avutu
; APPLICANT: Shukla, Vipula
; APPLICANT: Crosley, Rodney
; TITLE OF INVENTION: Nucleic Acid Compositions Confering Altered Metabolic Characteristics
; FILE REFERENCE: DOM-08552
; CURRENT APPLICATION NUMBER: US/10/487,901
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 7560
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2760
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-487-901-2760

```

```

Query Match          3.3%; Score 73; DB 94; Length 719;
Best Local Similarity 100.0%; Pred. No. 2,3e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1022 AGGAGGCATCCAGCCCAAGAGGGAGAGACCAAGGACACCGGACTTAGCAAAAGCCGA 1081
Db       7   AGGAGGCATCCAGCCCAAGAGGGAGAGACCAAGGACACCGGACTTAGCAAAAGCCGA 66

QY      1082 GCGACCGCGCTTCT 1094
Db       67 GCGACCGCGCTTCT 79

RESULT 6
US-10-487-901-6610
; Sequence 6610, Application US/10487901
; Publication No. US20050091708A1
; GENERAL INFORMATION:

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Query Match	3.3%;	Score 73;	DB 7;	Length 808;
Best Local Similarity	100.0%;	Pred. No.	2.3e-24;	

FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/1

RESULT 13
US-10-011-672-14
Sequence 14, Application US/10011672
Publication No. US2003004981A1
GENERAL INFORMATION:
APPLICANT: Hawkes, Timothy
APPLICANT: Warner, Simon
APPLICANT: Andrews, Christopher
APPLICANT: Bachoo, Satinder
APPLICANT: Pickerill, Andrew
TITLE OF INVENTION: HERBICIDE RESISTANT PLANTS
FILE REFERENCE: 50489/UST
CURRENT APPLICATION NUMBER: US/10/011,672
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: PCT/GB00/01559
PRIOR FILING DATE: 2000-04-20

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/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 14
/ LENGTH: 48
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Primer
US-10-011-672-14
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Query Match          1.3%; Score 29; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AATCCGAAAAGTTCTGCACCGTTTTCAC 29
Db      19 AATCCGAAAAGTTCTGCACCGTTTTCAC 47
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```
RESULT 14
US-10-012-070A-17
/ Sequence 17, Application US//10012070A
/ Publication No. US20030077801A1
/ GENERAL INFORMATION:
/ APPLICANT: Hawkes, Timothy
/ APPLICANT: Warner, Simon
/ APPLICANT: Andrews, Christopher
/ APPLICANT: Bachoo, Savinder
/ APPLICANT: Pickerill, Andrew
/ TITLE OF INVENTION: Herbicide Resistant Plants
/ FILE REFERENCE: 50490/US
/ CURRENT APPLICATION NUMBER: US/10/012,070A
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: PCT/GB00/01573
/ PRIOR FILING DATE: 2000-04-20
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 17
/ LENGTH: 48
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:primer
US-10-012-070A-17
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```
Query Match          1.3%; Score 29; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 AATCCGAAAAGTTCTGCACCGTTTTCAC 29
Db      19 AATCCGAAAAGTTCTGCACCGTTTTCAC 47
```

```
RESULT 15
US-10-311-455-63
/ Sequence 63, Application US//10311455
/ Publication No. US20030143606A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIEPENBROCK, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining Cytosine Methylation
/ FILE REFERENCE: 5013.1014
/ CURRENT APPLICATION NUMBER: US/10/311,455
/ PRIOR FILING DATE: 2002-12-16
/ PRIOR APPLICATION NUMBER: PCT/EP01/07537
/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
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/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 63
/ LENGTH: 12733
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-63
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Query Match          1.2%; Score 27; DB 6; Length 12733;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      333 AGAGAGATATTTTTTTTTTAAAAAAA 359
Db      1915 AGAGAGATATTTTTTTTTTAAAAAAA 1941
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Search completed: April 21, 2006, 10:06:15
Job time : 2647 secs
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 241 TCTGTCATGAAAGTTAAATTAATTCGAGTGGCCATTAATTCACAACCTCTCTTGAATA 300
 301 AAAAAATCTTTAGCTGAACTCAATGGGTAAGAGATATTTTTTTTTAAAAAAT 360
 301 AAAAAATCTTTAGCTGAACTCAATGGGTAAGAGATATTTTTTTTTAAAAAAT 360
 361 AGAATGAGATATTTCTGAAAGTATCGGCAAAAGATTTAAACATTAATTAATTTAT 420
 361 AGAATGAGATATTTCTGAAAGTATCGGCAAAAGATTTAAACATTAATTAATTTAT 420
 421 AGTTTGTGATTCGTATATATCGACGTCAATTAAGAGATGTCTTACTCCATCTCAATTT 480
 421 AGTTTGTGATTCGTATATATCGACGTCAATTAAGAGATGTCTTACTCCATCTCAATTT 480
 481 TATTTAGTAATTAAGACATTTGATTTATTTATTTATTTATTTTTCGATTAATGC 540
 481 TATTTAGTAATTAAGACATTTGATTTATTTATTTATTTATTTTTCGATTAATGC 540
 541 AAGGTAATTACGACACACTTTGTGCTCATGTGCATGTGAGTGCACCTCTCATACAC 600
 541 AAGGTAATTACGACACACTTTGTGCTCATGTGCATGTGAGTGCACCTCTCATACAC 600
 601 GTTCAACTGCGACACATCTCCAAATATCACTCGCTTAATTAATCAATTAAGTGAATA 660
 601 GTTCAACTGCGACACATCTCCAAATATCACTCGCTTAATTAATCAATTAAGTGAATA 660
 661 TCGAATTCAGACATTCACATCAACAGACCACTTTTAATTAATCTAAATACAAAA 720
 661 TCGAATTCAGACATTCACATCAACAGACCACTTTTAATTAATCTAAATACAAAA 720
 721 ATTAATTTAAGAAATGATGAAAGATGAAAGATGAAAGATTAATTAATTAATTAATTA 780
 721 ATTAATTTAAGAAATGATGAAAGATGAAAGATGAAAGATTAATTAATTAATTAATTA 780
 781 AAAAAAAGATTTTGTGCTGTGCGGAGGCGCAATCTCCATATTTGGGCAACAGGCA 840
 781 AAAAAAAGATTTTGTGCTGTGCGGAGGCGCAATCTCCATATTTGGGCAACAGGCA 840
 841 CAACAGATGGGCGCCACAGAACCAACCAAAACAGATCTTAACGAGAGACAGCA 900
 841 CAACAGATGGGCGCCACAGAACCAACCAAAACAGATCTTAACGAGAGACAGCA 900
 901 AGTCCGCAACACTTTTAAAGCAGGCTTTGGCGCAGAGAGAGAGAGAGAGGCAAG 960
 901 AGTCCGCAACACTTTTAAAGCAGGCTTTGGCGCAGAGAGAGAGAGAGAGGCAAG 960
 961 AAAAAAGATTCCTCTCTCCATCTTAATTTCTCTCCCTTTTCCCTCTCTATA 1020
 961 AAAAAAGATTCCTCTCTCCATCTTAATTTCTCTCCCTTTTCCCTCTCTATA 1020
 1021 TGAAGGATTCAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 1021 TGAAGGATTCAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 1081 AGCGACCGGCTTCTTCATCATATCTTCGAGTCTGATCTTGGTGCATCTCTCCCTC 1140
 1081 AGCGACCGGCTTCTTCATCATATCTTCGAGTCTGATCTTGGTGCATCTCTCCCTC 1140
 1141 TCGACTCTCTCTCACAGGATATGCTTGGTGTCTTGGATTTATGTTCTAGGT 1200
 1141 TCGACTCTCTCTCACAGGATATGCTTGGTGTCTTGGATTTATGTTCTAGGT 1200
 1201 TGTGTATGATCGGCGTGTATGTTAGAAAGGGGATCTGTATCTGTATGATCTCTGCT 1260
 1201 TGTGTATGATCGGCGTGTATGTTAGAAAGGGGATCTGTATCTGTATGATCTCTGCT 1260
 1261 TGGATTTGGGATGAGAGGGGCTTTGATGTTGATGATGATGATGATGATGATGATGAT 1320
 1261 TGGATTTGGGATGAGAGGGGCTTTGATGTTGATGATGATGATGATGATGATGATGAT 1320
 1321 ATGCTTTCAATCGTCTGAGAGCTTAATGAAATGATTAAGGATCGGAATCTT 1380
 1321 ATGCTTTCAATCGTCTGAGAGCTTAATGAAATGATTAAGGATCGGAATCTT 1380

Db 1321 ATGCTTTCAATCGTCTGAGAGCTTAATGAAATGATTAAGGATCGGAATCTT 1380
 Qy 1381 GCGATTTTGTAGATCACTTTTGTGAGGTAAATCAAGACACCGGTGATTTGCTGGT 1440
 Db 1381 GCGATTTTGTAGATCACTTTTGTGAGGTAAATCAAGACACCGGTGATTTGCTGGT 1440
 Qy 1441 GTTAATTAAGATGATTTGTTGCTGCTGATCTGTGATGATGCTTCTCAATTTGACGA 1500
 Db 1441 GTTAATTAAGATGATTTGTTGCTGCTGATCTGTGATGATGCTTCTCAATTTGACGA 1500
 Qy 1501 AGCTATCCCTTTGTTATTTCCCATTAAGCAAAAAATTAATCAACTTTGAAGACGTCCT 1560
 Db 1501 AGCTATCCCTTTGTTATTTCCCATTAAGCAAAAAATTAATCAACTTTGAAGACGTCCT 1560
 Qy 1561 TGATGAGATGATGATTTGATTTTCAAGCTGTCCAAATTTTCGAGCTGGCTGTTAG 1620
 Db 1561 TGATGAGATGATGATTTGATTTTCAAGCTGTCCAAATTTTCGAGCTGGCTGTTAG 1620
 Qy 1621 ATACAGTATGATGATTTGATTTTCAAGCTGTCCAAATTTTCGAGCTGGCTGTTAG 1680
 Db 1621 ATACAGTATGATGATTTGATTTTCAAGCTGTCCAAATTTTCGAGCTGGCTGTTAG 1680
 Qy 1681 TCCCTGTTCTTCCGATTTGCTTGTAGTCCAGAAATTTTTCCTCAAAATATCTTAAAGT 1740
 Db 1681 TCCCTGTTCTTCCGATTTGCTTGTAGTCCAGAAATTTTTCCTCAAAATATCTTAAAGT 1740
 Qy 1741 CACTTCTGTTTCACTTCAATGATTAATGATGATGATGATGATGATGATGATGATGAT 1800
 Db 1741 CACTTCTGTTTCACTTCAATGATTAATGATGATGATGATGATGATGATGATGATGAT 1800
 Qy 1801 TAGCTGTATGATGATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 1860
 Db 1801 TAGCTGTATGATGATTTATGATTAATGATTAATGATTAATGATTAATGATTAATGAT 1860
 Qy 1861 GATTTCTGATCCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1920
 Db 1861 GATTTCTGATCCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1920
 Qy 1921 GATTTCTGATCCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1980
 Db 1921 GATTTCTGATCCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1980
 Qy 1981 ACTGTCTCAATTTTGTGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
 Db 1981 ACTGTCTCAATTTTGTGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040
 Qy 2041 TACCTGTATGATTTCTTTTGTGATTTCTTGAATCTTGAATCTTGAATCTTGAATCTT 2100
 Db 2041 TACCTGTATGATTTCTTTTGTGATTTCTTGAATCTTGAATCTTGAATCTTGAATCTT 2100
 Qy 2101 GAAAGCTGTATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Db 2101 GAAAGCTGTATGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
 Qy 2161 CTGGTGTATGATGATTTGATTTTCAAGCTTTTCAAGCTTTTCAAGCTTTTCAAGCT 2195
 Db 2161 CTGGTGTATGATGATTTGATTTTCAAGCTTTTCAAGCTTTTCAAGCTTTTCAAGCT 2195

RESULT 2
 US-11-128-549-2
 ; Sequence 2, Application US/11128549
 ; Publication No. US20050262597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Broekaert, Willem
 ; APPLICANT: De Wilde, Chris
 ; APPLICANT: Hatfeld, Yves
 ; APPLICANT: Zhou, Zhongyi
 ; TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION
 ; FILE REFERENCE: 1187-40
 ; CURRENT APPLICATION NUMBER: US/11/128,549
 ; PRIORITY FILING DATE: 2005-05-13
 ; PRIOR APPLICATION NUMBER: US 60/572,141

Db	306	GGAAATCTTGCGATTTTGTGAGTACTTTTGTGTTAGAGTAAATCAGAGCACCGGTGATTT	365
Qy	1433	TGCTTGTGTATATAAAGTACATTTGTTTGCTCTCGATTCGTGAGTATGCTTTCTGA	1492
Db	366	TGCTTGATGTATATAAAGTACAGGTGTTTGGTCTCGATTCGTGAGTATGCTTTCTGA	425
Qy	1493	TTTGACGAAGCTATCTTTGTTTATTTCCCTATGTAACAAAAATATCCACTTTGGAAGAC	1552
Db	426	TTTTCGAGAGCTATCTTTGTTTATTTCCCTATGTAACAAAAATATCCACTTTGGAAGAC	485
Qy	1553	GGTCCCGTTGATGAGATGGAATGATTTGATCTTAAAGCTGTCCAAAATTTGCGAGCTGGC	1612
Db	486	GGTCCCGTTGATGAGATGGAATGATTTGATCTTAAAGCTGTCCAAAATTTGCGAGCTGGC	545
Qy	1613	TTGTTTAGATACAGTAGTCCCCATCAGCAAAATTCATGTAAAAACAGTTATATCTCAGGAA	1672
Db	546	TTGTTTAGATACAGTAGTCCCCATCAGCAAAATTCATGTAAAAACAGTTATATCTCAGGAA	605
Qy	1673	CAGGGGATTCCTCTGTCTTCCGATTTGCTTTATGTCCAGAAATTTTTCCTCCAAATATCT	1732
Db	606	CAGGGGATTCCTCTGTCTTCCGATTTGCTTTATGTCCAGAAATTTTTCCTCCAAATATCT	665
Qy	1733	TAAAAAGTCACTTTCGTGTTCAGTTCATGSAATTTGATGCTACAAATATAGCTTTTATAG	1792
Db	666	TAAAAAGTCACTTTCGTGTTCAGTTCATGSAATTTGATGCTACAAATATAGCTTTTATAG	725
Qy	1793	CGTTATCTTACCTGTAGTTCAAGTTATAGTAAATACCCCTATAGTTTGTGAGAGAGA	1852
Db	726	CGTTATCTTACCTGTAGTTCAAGTTATAGTAAATACCCCTATAGTTTGTGAGAGAGA	785
Qy	1853	ACTTATCCGATTTCTGATCTCCATTTTATATATATGAAATGAACCTGATAGACAGAGT	1912
Db	786	ACTTATCCGATTTCTGATCTCCATTTTATATATATGAAATGAACCTGATAGACAGAGT	845
Qy	1913	ATTGATTTGGATATTTTTTTTATATAGCTTTCACCCCTTCAATATATCTGACCTGAAAGTC	1972
Db	846	ATTGATTTGGATATTTTTTTTATATAGCTTTCACCCCTTCAATATATCTGACCTGAAAGTC	905
Qy	1973	TGGCATGAACTGCTCTCAATTTTGTTTCAATTCACATTCGATATATCATGATGATATCT	2032
Db	906	TGGCATGAACTGCTCTCAATTTTGTTTCAATTCACATTCGATATATCATGATGATATCT	965
Qy	2033	CTTGATCTTACCTGTAGAAAGTTCTTTTGGTTATTCCTTGAAGCTGTGATTAAGAAG	2092
Db	966	CTTGATCTTACCTGTAGAAAGTTCTTTTGGTTATTCCTTGAAGCTGTGATTAAGAAG	1025
Qy	2093	AAATTTATGAAGCTGTAAATCGGAAATGTTATACCTGCTGTTCTTATGATTAATTTCTTT	2152
Db	1026	AAATTTATGAAGCTGTAAATCGGAAATGTTATACCTGCTGTTCTTATGATTAATTTCTTT	1085
Qy	2153	GTGACGTTCTGTGTAGCTTGCCACT	2179
Db	1086	GTGACGTTCTGTGTAGCTTGCCACT	1112

RESULT 4
US-11-128-549-5
Sequence 5, Application US/11128549
Publication No. US20050262597A1
GENERAL INFORMATION:
APPLICANT: Broekaert, Willem
APPLICANT: De Wilde, Chris
APPLICANT: Hatzfeld, Yves
APPLICANT: Zhou, Zhongyi
TITLE OF INVENTION: METHOD FOR INCREASING TRANSGENE EXPRESSION
FILE REFERENCE: 1187-40
CURRENT APPLICATION NUMBER: US/11/128, 549
CURRENT FILING DATE: 2005-05-13
PRIORITY APPLICATION NUMBER: US 60/572,141
PRIORITY FILING DATE: 2004-05-18
PRIORITY APPLICATION NUMBER: EP 04102108.0
PRIORITY FILING DATE: 2004-05-13

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Oryza sativa
US-11-128-549-5

```

Query Match	29.2%	Score 642;	DB 14;	Length 999;
Best Local Similarity	99.3%	Pred. NO. 2e-275;		
Matches 992; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	1160	GTATGTCGCCCTCGSTGTTCTTGGAATTTATGTTCTTAGAGTGTGTAACAGGGCGTTGA	1215
Db	1	GTATGTCGCCCTCGSTGTTCTTGGAATTTATGTTCTTAGAGTGTGTAACAGGGCGTTGA	60
QY	1220	TGTTAGGAAAGAGGGGATCTGATCTGTGATGATTCCTGTTCTTGGAATTTGGGATAGAGGG	1275
Db	61	TGTTAGGAAAGAGGGATCTGATCTGTGATGATTCCTGTTCTTGGAATTTGGGATAGAGGG	120
QY	1280	TTCTTGATGTTGCATGTTATCGGTTCCGTTTGATTAGTATGATGTTTCAATGCTCTGG	1335
Db	121	TTCTTGATGTTGCATGTTATCGGTTCCGTTTGATTAGTATGATGTTTCAATGCTCTGG	180
QY	1340	AGACTCTATGGAATGAAATGTTAGTTAGGGTAACGAATCTGGCATTTTGGAGTAACTT	1395
Db	181	AGACTCTATGGAATGAAATGTTAGGGTAACGAATCTGGCATTTTGGAGTAACTT	240
QY	1400	TTGTTTGAAGTAATCAGAGCACCGGATTTTGTCTGTGTAATAAAGTACATTTGT	1455
Db	241	TTGTTTGAAGTAATCAGAGCACCGGATTTTGTCTGTGTAATAAAGTACATTTGT	300
QY	1460	TTGGTCTCGATTCGTGTAATGATGCTTCTCGATTTGACGAGCTATCCTTTGTTATTC	1515
Db	301	TTGGTCTCGATTCGTGTAATGATGCTTCTCGATTTGACGAGCTATCCTTTGTTATTC	360
QY	1520	CCATATTGAACAAAATAATCCACTTTGGAACAGGTCCTCCCTGATGATGATGATGATG	1575
Db	361	CCATATTGAACAAAATAATCCACTTTGGAACAGGTCCTCCCTGATGATGATGATGATG	420
QY	1580	ATTCTTAAAGCCTGTCCAAAATTTGGCAGCTGGCTGTTAGATACAGATGCCCATCAC	1635
Db	421	ATTCTTAAAGCCTGTCCAAAATTTGGCAGCTGGCTGTTAGATACAGATGCCCATCAC	480
QY	1640	GAAATTCATGAAAACAGTTATATCTCTCAGAACAGGGATTCCTGTCTTCGATTTGG	1695
Db	481	GAAATTCATGAAAACAGTTATATCTCTCAGAACAGGGATTCCTGTCTTCGATTTGG	540
QY	1700	CTTTAGTCCCGAATTTTTTTCCTCCAAATATCTTAAAAAGTCATTTCTGGTTCACTCA	1755
Db	541	CTTTAGTCCCGAATTTTTTTCCTCCAAATATCTTAAAAAGTCATTTCTGGTTCACTCA	600
QY	1760	ATGAATTGATGTGCATACAAATAATGCTTTATAGCGTATCCTAGCTGATGTCAGTTAT	1815
Db	601	ATGAATTGATGTGCATACAAATAATGCTTTATAGCGTATCCTAGCTGATGTCAGTTAT	660
QY	1820	AGTAATATACCCCTATAGTTTAGTCAAGAGAAAGAACTTATCCGATTTCTGATCTCCATTT	1875
Db	661	AGTAATATACCCCTATAGTTTAGTCAAGAGAAAGAACTTATCCGATTTCTGATCTCCATTT	720
QY	1880	TAAATTATATGAATGAAGTAAGTAAGCACTAAGCACTATCAATTGGATATTTTTTTTATAG	1935
Db	721	TAAATTATATGAATGAAGTAAGTAAGCACTAAGCACTATCAATTGGATATTTTTTTTATAG	780
QY	1940	CTTTCACCCCTCAATTAATCTGAGCTGAAATCTGGGCAATGAACGTCTCAATTTGTTT	1995
Db	781	CTTTCACCCCTCAATTAATCTGAGCTGAAATCTGGGCAATGAACGTCTCAATTTGTTT	840
QY	2000	TCAATTCACATCGATTTATCTATGATTAATCCTCTTGATCTTACCTGTAGAAATTTCTTT	2055
Db	841	TCAATTCACATCGATTTATCTATGATTAATCCTCTTGATCTTACCTGTAGAAATTTCTTT	900
QY	2060	TTGGTATATCTTGATCTGCTGATTTACAGAAAGAAATTTATGAAAGCTGTAATCCGGATAG	2115

Db 901 TTGGTATTCCTTGACGCTTGATTCACGAAGAAATTTATGAAGCTGATATCGGATAG 960
Qy 2120 TTATACGCTTGCTTCTATGATTCATTCCTTTGTGCG 2158
961 TTATACGCTTGCTTCTATGATTCATTCCTTTGTGCG 999

RESULT 5

US-09-925-065A-795898/c
; Sequence 795898, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 795898
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-795898

Query Match 1.0%; Score 22; DB 6; Length 378;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 772 CACATACAAAAAAGAAAT 793
Db 353 CACATACAAAAAAGAAAT 332

RESULT 6

US-09-925-065A-795899/c
; Sequence 795899, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 795899
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-795899

Query Match 1.0%; Score 22; DB 6; Length 567;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 772 CACATACAAAAAAGAAAT 793
Db 223 CACATACAAAAAAGAAAT 202

RESULT 7

US-09-925-065A-685691/c
; Sequence 685691, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685691
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-685691

Query Match 1.0%; Score 22; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 337 AGATATTTTTTTTTAAAAA 358
Db 198 AGATATTTTTTTTTAAAAA 177

RESULT 8

US-09-925-065A-684849
; Sequence 684849, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 684849

LENGTH: 1219
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-664849

Query Match 1.0%; Score 22; DB 6; Length 1219;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 779 AAAAAAAAAAGATTGCTC 800
|||||
Db 612 AAAAAAAAAAGATTGCTC 633

RESULT 9
US-09-925-065A-92058/c
Sequence 92058, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 92058
LENGTH: 1296
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-92058

Query Match 1.0%; Score 22; DB 6; Length 1296;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 CACATACCAAAAAAAAAAGAT 793
|||||
Db 223 CACATACCAAAAAAAAAAGAT 202

RESULT 10
US-10-301-480-193300/c
Sequence 193300, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 193300
LENGTH: 1296
TYPE: DNA
ORGANISM: Homo sapiens

US-10-301-480-193300

Query Match 1.0%; Score 22; DB 9; Length 1296;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 CACATACCAAAAAAAAAAGAT 793
|||||
Db 223 CACATACCAAAAAAAAAAGAT 202

RESULT 11
US-10-301-480-806709/c
Sequence 806709, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 806709
LENGTH: 1296
TYPE: DNA
ORGANISM: Homo sapiens
US-10-301-480-806709

Query Match 1.0%; Score 22; DB 10; Length 1296;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 772 CACATACCAAAAAAAAAAGAT 793
|||||
Db 223 CACATACCAAAAAAAAAAGAT 202

RESULT 12
US-10-541-315-1/c
Sequence 1, Application US/10541315
Publication No. US20060053507A1
GENERAL INFORMATION:
APPLICANT: CropDesign N.V.
TITLE OF INVENTION: Regulatory sequence
FILE REFERENCE: CD-072-PCT
CURRENT APPLICATION NUMBER: US/10/541,315
PRIOR FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: EP 03075207.5
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2195
TYPE: DNA
ORGANISM: Oryza sativa
US-10-541-315-1

Query Match 1.0%; Score 22; DB 9; Length 2195;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 340 TATTTTTTTTTTAAAAAAAAATA 361
|||||
Db 361 TATTTTTTTTTTAAAAAAAAATA 340

RESULT 13


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US-10-240-708-56/c
; Sequence 56, Application US/10240708
; Publication No. US20050282157A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPERROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/240,708
; PRIOR FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 56
; LENGTH: 11015
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-56

Query Match
Best Local Similarity 1.0%; Score 22; DB 8; Length 11015;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 700 ATATATCTAAATACAAAAA 721
DB 2698 ATATATCTAAATACAAAAA 2677

RESULT 14
US-11-121-086-38/c
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 151169
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-38

Query Match
Best Local Similarity 1.0%; Score 22; DB 14; Length 151169;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 AGATATTTTTTTTAAAAAAA 358
DB 107567 AGATATTTTTTTTAAAAAAA 107546

RESULT 15
US-09-925-065A-110555/c
; Sequence 110555, Application US/09925065A
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110555
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-110555

Query Match
Best Local Similarity 1.0%; Score 21; DB 6; Length 369;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 ATATTTTTTTTTTAAAAAAA 359
DB 183 ATATTTTTTTTTTAAAAAAA 163
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Search completed: April 21, 2006, 11:25:53
Job time : 5934 secs

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